

SCORE Search Results Details for Application 10753267 and Search Result 20070205_152801_us-10-753-267-20.rapbn.

Score Home Page Batchwise Annotation List SCORE System Database SCORE EAD Comments / Suggestions

This page gives you Search Results detail for the Application 10753267 and Search Result 20070205_152801_us-10-753-267-20.rapbn.

Start

Go Back to previous page

GenCore version 6.2
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OM protein - protein search, using sw model
Run on: February 6, 2007, 06:03:24 : Search time 61 Seconds
(Without alignments)
661,445 Million cell updates/sec

Title: US-10-753-267-20
Perfect score: 1649
Sequence: 1 MATHESVIFSSASLAVYV.....TDSQNYVYHKKRFEKTE 293
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 571941 seqs, 137706945 residues
Total number of hits satisfying chosen parameters: 571941
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 01
Maximum Match 1001
Listing first 45 summaries

Databases :
1: /BNC_Celerra_S1053/pcoddata/1/pubseq/us09_NEW_PUB pep.*
2: /BNC_Celerra_S1053/pcoddata/1/pubseq/us06_NEW_PUB pep.*
3: /BNC_Celerra_S1053/pcoddata/1/pubseq/us07_NEW_PUB pep.*
4: /BNC_Celerra_S1053/pcoddata/1/pubseq/us08_NEW_PUB pep.*
5: /BNC_Celerra_S1053/pcoddata/1/pubseq/pct_NEW_PUB pep.*

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=110556&ItemName=20070205_152801_us-10-753-267-20.rapbn. 2/8/07

Query Match
Query Match Similarity 100.0%: Pred. No. 1,66-146; Indels 0; Gaps 0;
Matches 293, Conservative 0, Mismatches 0

Sequence 3035, Ap
Sequence 1389, Ap
Sequence 2149, Ap
Sequence 2349, Ap
Sequence 6495, Ap
Sequence 7771, Ap
Sequence 2097, Ap
Sequence 6124, Ap
Sequence 6462, A
Sequence 13016, A
Sequence 3447, Ap
Sequence 11863, A

Sequence 3035, Ap
Sequence 1389, Ap
Sequence 2149, Ap
Sequence 2349, Ap
Sequence 6495, Ap
Sequence 7771, Ap
Sequence 2097, Ap
Sequence 6124, Ap
Sequence 6462, A
Sequence 13016, A
Sequence 3447, Ap
Sequence 11863, A

RESULT 1
US-10-533-519-1389
Sequence 1389, Application US/10533519
GENERAL INFORMATION:
PUBLICATION NO. US2006026377A1
APPLICANT: CLARK HENRY
APPLICANT: CLARK HENRY
APPLICANT: VANLOOKE MESSNO
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WOOD, THOMAS D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
RELATED DISEASES
TITLE OF INVENTION: RELATED DISEASES
PCT NUMBER: US/03/519
CURRENT APPLICATION NUMBER: US/10/533,519
PRIOR FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: PCT/US03/14312
PRIOR FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 60/423,394
PRIOR FILING DATE: 2002-11-01
PCT ID NOS: 2317
SEQ ID NOS: 231
LENGTH: 233
TYPE: PRT
ORGANISM: Homo sapien
US-10-533-519-1389

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=110556&ItemName=20070205_152801_us-10-753-267-20.rapbn. 2/8/07

6: /BNC_Celerra_S1053/pcoddata/1/pubseq/us10_NEW_PUB pep.*
7: /BNC_Celerra_S1053/pcoddata/1/pubseq/us11_NEW_PUB pep.*
8: /BNC_Celerra_S1053/pcoddata/1/pubseq/us60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result	No.	Score	Match Length	Description
1	1649	100.0	293	US-10-533-519-1389 Sequence 1389, Ap
2	1649	100.0	293	US-10-528-2608-163 Sequence 163, Ap
3	1649	100.0	293	US-10-518-0518-2382 Sequence 2382, Ap
4	1649	100.0	293	US-10-518-0518-2382 Sequence 2382, Ap
5	1477	89.6	293	US-10-518-0518-2380 Sequence 2380, Ap
6	918	55.7	162	US-10-537-121-123 Sequence 123, Ap
7	593	36.0	317	US-10-449-902-39207 Sequence 39207, A
8	584	35.4	313	US-11-330-403-13559 Sequence 13559, A
9	582	35.3	305	US-11-330-403-17376 Sequence 17376, A
10	546.5	33.3	284	US-11-330-403-12213 Sequence 12213, A
11	546.5	33.3	284	US-11-330-403-12213 Sequence 12213, A
12	542.5	32.9	291	US-11-330-403-8653 Sequence 8653, Ap
13	542.5	32.9	291	US-11-330-403-8653 Sequence 8653, Ap
14	541	32.8	318	US-11-520-715-61110 Sequence 61110, A
15	541	32.8	318	US-11-520-715-61110 Sequence 61110, A
16	540	32.7	311	US-11-520-715-47836 Sequence 47836, A
17	539.5	32.7	284	US-11-330-403-2893 Sequence 2893, Ap
18	539.5	32.7	284	US-11-330-403-2893 Sequence 2893, Ap
19	539.5	32.7	268	US-11-330-403-8791 Sequence 8791, A
20	539.5	32.7	268	US-11-330-403-8791 Sequence 8791, A
21	538.5	32.7	268	US-11-330-403-9060 Sequence 9060, Ap
22	538.5	32.7	306	US-11-330-403-13598 Sequence 13598, A
23	537.5	32.6	266	US-11-330-403-15543 Sequence 15543, A
24	536.5	32.5	309	US-11-330-403-15021 Sequence 15021, A
25	536.5	32.5	309	US-11-330-403-15021 Sequence 15021, A
26	536.5	32.5	309	US-11-330-403-15021 Sequence 15021, A
27	528	32.0	266	US-10-449-902-5824 Sequence 5824, A
28	528	32.0	266	US-10-449-902-5824 Sequence 5824, A
29	518	31.4	300	US-11-330-403-12774 Sequence 12774, A
30	517.5	31.4	309	US-11-330-403-11660 Sequence 11660, A
31	515	31.2	269	US-11-330-403-4749 Sequence 4749, Ap
32	513	31.1	261	US-11-330-403-4749 Sequence 4749, Ap

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=110556&ItemName=20070205_152801_us-10-753-267-20.rapbn. 2/8/07

Query Match
Query Match Similarity 100.0%: Pred. No. 1,66-146; Indels 0; Gaps 0;
Matches 293, Conservative 0, Mismatches 0

Sequence 3035, Ap
Sequence 1389, Ap
Sequence 2149, Ap
Sequence 2349, Ap
Sequence 6495, Ap
Sequence 7771, Ap
Sequence 2097, Ap
Sequence 6124, Ap
Sequence 6462, A
Sequence 13016, A
Sequence 3447, Ap
Sequence 11863, A

Sequence 3035, Ap
Sequence 1389, Ap
Sequence 2149, Ap
Sequence 2349, Ap
Sequence 6495, Ap
Sequence 7771, Ap
Sequence 2097, Ap
Sequence 6124, Ap
Sequence 6462, A
Sequence 13016, A
Sequence 3447, Ap
Sequence 11863, A

RESULT 2
US-10-528-2608-163
Sequence 163, Application US/105282608
PUBLICATION NO. US2007010434A1
GENERAL INFORMATION:
PUBLICATION NO. US2007010434A1
APPLICANT: CLARK HENRY
APPLICANT: CLARK HENRY
APPLICANT: VANLOOKE MESSNO
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WOOD, THOMAS D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING IMMUNE DISORDERS
TITLE OF INVENTION: RELATED DISEASES
PCT NUMBER: US/10/528,2608
CURRENT APPLICATION NUMBER: US/10/528,2608
PRIOR FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US 60/411,392
PRIOR FILING DATE: 2002-09-16
PCT ID NOS: 2317
SEQ ID NOS: 231
LENGTH: 233
TYPE: PRT
ORGANISM: Homo sapien
US-10-533-519-1389

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=110556&ItemName=20070205_152801_us-10-753-267-20.rapbn. 2/8/07

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1 NUMBER OF SEQ ID NOS: 506
2 SEQ ID NO 143
3 LENGTH: 293
4 TYPE: PRT
5 ORGANISM: Homo sapiens
US-10-528-2608-163

Query Match
Best Local Similarity 100.0% Score 1649; DB 6; Length 293;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Dy 61 LVFLPCLPGLPQIPFNKKYKIQKDETEWQKCFVLLPNHFCIQPLICGTYTFT 120
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Dy 121 EYFNIPYDEMPPRYFTLLARCGCAVIEDTHYFHLRLHHRIYKYHKVHIEPQPF 180
Oy 181 GNEAYNPLETLILGTGPFQIGVLLCDHVLNMMVTLLETIDWISGYDIFLPLNL 240
Dy 181 GNEAYNPLETLILGTGPFQIGVLLCDHVLNMMVTLLETIDWISGYDIFLPLNL 240
Oy 241 IFFYAGSRHHDHNNFTIGNYASTFTFWMDRIFGDSQYWAYNEKKRKEKTE 293
Dy 241 IFFYAGSRHHDHNNFTIGNYASTFTFWMDRIFGDSQYWAYNEKKRKEKTE 293

RESULT 3
US-10-219-0518-2382
1 Sequence 2382, Application US/102190518
2 Publication No. US20070015145A1
3 APPLICANT: The General Hospital Corporation doing business as Massachusetts General
4 APPLICANT: Hospital / Bayer AG
5 TITLE OF INVENTION: Identifying matched biological reagents and methods for
6 TITLE OF INVENTION: IDENTIFYING MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
7 FILE REFERENCE: Inv-1005-UT2
8 CURRENT APPLICATION NUMBER: US/11/371,354
9 PRIOR FILING DATE: 2006-03-07
10 PRIOR APPLICATION NUMBER: 60/673,045
11 PRIOR FILING DATE: 2005-03-25
12 PRIOR APPLICATION NUMBER: 60/665,199
13 PRIOR FILING DATE: 2005-03-25
14 PRIOR APPLICATION NUMBER: 60/665,200
15 PRIOR FILING DATE: 2005-03-25
16 PRIOR APPLICATION NUMBER: 60/659,493
17 PRIOR FILING DATE: 2005-03-07
18 PRIOR APPLICATION NUMBER: 60/659,492
19 PRIOR FILING DATE: 2005-02-15
20 PRIOR APPLICATION NUMBER: 60/653,586
21 PRIOR FILING DATE: 2005-02-15
22 PRIOR APPLICATION NUMBER: 60/651,390
23 PRIOR FILING DATE: 2005-02-08
24 NUMBER OF SEQ ID NOS: 78682
25 SOFTWARE: Patent version 3.3
26 SEQ ID NO 143
27 LENGTH: 293
28 TYPE: PRT
29 ORGANISM: Homo sapiens
US-11-371-334-75335
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http://es/ScoreAccessWeb/GelItem.action?AppId=10753267&seqId=110556&ItemName=20070205_152801_us-10-753-267-20.rnphn 28/07

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1 APPLICANT: CARILLO, JOHN
2 APPLICANT: Hospital / Bayer AG
3 TITLE OF INVENTION: IDENTIFYING MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
4 TITLE OF INVENTION: IDENTIFYING MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
5 FILE REFERENCE: Inv-1005-UT2
6 CURRENT APPLICATION NUMBER: US/11/371,354
7 PRIOR FILING DATE: 2006-03-07
8 PRIOR APPLICATION NUMBER: 60/673,045
9 PRIOR FILING DATE: 2005-03-25
10 PRIOR APPLICATION NUMBER: 60/665,199
11 PRIOR FILING DATE: 2005-03-25
12 PRIOR APPLICATION NUMBER: 60/665,200
13 PRIOR FILING DATE: 2005-03-25
14 PRIOR APPLICATION NUMBER: 60/659,493
15 PRIOR FILING DATE: 2005-03-07
16 PRIOR APPLICATION NUMBER: 60/659,492
17 PRIOR FILING DATE: 2005-02-15
18 PRIOR APPLICATION NUMBER: 60/653,586
19 PRIOR FILING DATE: 2005-02-15
20 PRIOR APPLICATION NUMBER: 60/651,390
21 PRIOR FILING DATE: 2005-02-08
22 NUMBER OF SEQ ID NOS: 78682
23 SOFTWARE: Patent version 3.3
24 SEQ ID NO 143
25 LENGTH: 293
26 TYPE: PRT
27 ORGANISM: Homo sapiens
US-11-371-334-75335

Query Match
Best Local Similarity 100.0% Score 1649; DB 7; Length 293;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MATHESVIFSSASLAVVEYDVLLENFQEPFNANNMLNUNYTKFQIATGSLVIEHA 60
Dy 1 MATHESVIFSSASLAVVEYDVLLENFQEPFNANNMLNUNYTKFQIATGSLVIEHA 60
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Dy 61 LVFLPCLPGLPQIPFNKKYKIQKDETEWQKCFVLLPNHFCIQPLICGTYTFT 120
Oy 121 EYFNIPYDEMPPRYFTLLARCGCAVIEDTHYFHLRLHHRIYKYHKVHIEPQPF 180
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1 PRIOR APPLICATION NUMBER: US 60/346,382
2 PRIOR FILING DATE: 2001-11-01
3 PRIOR APPLICATION NUMBER: US 60/333,347
4 PRIOR FILING DATE: 2001-11-26
5 NUMBER OF SEQ ID NOS: 14715
6 SOFTWARE: Perl script
7 SEQ ID NO 2382
8 LENGTH: 293
9 TYPE: PRT
10 ORGANISM: Homo sapiens
US-10-219-0518-2382

Query Match
Best Local Similarity 100.0% Score 1649; DB 6; Length 293;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Dy 1 MATHESVIFSSASLAVVEYDVLLENFQEPFNANNMLNUNYTKFQIATGSLVIEHA 60
Oy 61 LVFLPCLPGLPQIPFNKKYKIQKDETEWQKCFVLLPNHFCIQPLICGTYTFT 120
Dy 61 LVFLPCLPGLPQIPFNKKYKIQKDETEWQKCFVLLPNHFCIQPLICGTYTFT 120
Oy 121 EYFNIPYDEMPPRYFTLLARCGCAVIEDTHYFHLRLHHRIYKYHKVHIEPQPF 180
Dy 121 EYFNIPYDEMPPRYFTLLARCGCAVIEDTHYFHLRLHHRIYKYHKVHIEPQPF 180
Oy 181 GNEAYNPLETLILGTGPFQIGVLLCDHVLNMMVTLLETIDWISGYDIFLPLNL 240
Dy 181 GNEAYNPLETLILGTGPFQIGVLLCDHVLNMMVTLLETIDWISGYDIFLPLNL 240
Oy 241 IFFYAGSRHHDHNNFTIGNYASTFTFWMDRIFGDSQYWAYNEKKRKEKTE 293
Dy 241 IFFYAGSRHHDHNNFTIGNYASTFTFWMDRIFGDSQYWAYNEKKRKEKTE 293

RESULT 4
US-11-371-334-75335
1 Sequence 75335, Application US/11/371,354
2 Publication No. US20060275794A1
3 GENERAL INFORMATION:
4 APPLICANT: The General Hospital Corporation doing business as Massachusetts General
5 APPLICANT: Hospital / Bayer AG
6 TITLE OF INVENTION: Identifying matched biological reagents and methods for
7 TITLE OF INVENTION: IDENTIFYING MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
8 FILE REFERENCE: Inv-1005-UT2
9 CURRENT APPLICATION NUMBER: US/11/371,354
10 PRIOR FILING DATE: 2006-03-07
11 PRIOR APPLICATION NUMBER: 60/673,045
12 PRIOR FILING DATE: 2005-03-25
13 PRIOR APPLICATION NUMBER: 60/665,199
14 PRIOR FILING DATE: 2005-03-25
15 PRIOR APPLICATION NUMBER: 60/665,200
16 PRIOR FILING DATE: 2005-03-25
17 PRIOR APPLICATION NUMBER: 60/659,493
18 PRIOR FILING DATE: 2005-03-07
19 PRIOR APPLICATION NUMBER: 60/659,492
20 PRIOR FILING DATE: 2005-02-15
21 PRIOR APPLICATION NUMBER: 60/653,586
22 PRIOR FILING DATE: 2005-02-15
23 PRIOR APPLICATION NUMBER: 60/651,390
24 PRIOR FILING DATE: 2005-02-08
25 NUMBER OF SEQ ID NOS: 14715
26 SOFTWARE: Perl script
27 SEQ ID NO 2382
28 LENGTH: 293
29 TYPE: PRT
30 ORGANISM: Homo sapiens
US-11-371-334-75335
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http://es/ScoreAccessWeb/GelItem.action?AppId=10753267&seqId=110556&ItemName=20070205_152801_us-10-753-267-20.rnphn 28/07

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Oy 241 IFFYAGSRHHDHNNFTIGNYASTFTFWMDRIFGDSQYWAYNEKKRKEKTE 293
Dy 241 IFFYAGSRHHDHNNFTIGNYASTFTFWMDRIFGDSQYWAYNEKKRKEKTE 293

RESULT 5
US-10-219-0518-2380
1 Sequence 2380, Application US/102190518
2 Publication No. US20070015145A1
3 GENERAL INFORMATION:
4 APPLICANT: The General Hospital Corporation doing business as Massachusetts General
5 APPLICANT: Hospital / Bayer AG
6 TITLE OF INVENTION: Identifying matched biological reagents and methods for
7 TITLE OF INVENTION: IDENTIFYING MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
8 FILE REFERENCE: Inv-1005-UT2
9 CURRENT APPLICATION NUMBER: US/10/219,0518
10 PRIOR FILING DATE: 2003-05-09
11 PRIOR APPLICATION NUMBER: US 60/312,147
12 PRIOR FILING DATE: 2001-08-14
13 PRIOR APPLICATION NUMBER: US 60/346,382
14 PRIOR FILING DATE: 2001-11-26
15 PRIOR APPLICATION NUMBER: US 60/333,347
16 PRIOR FILING DATE: 2001-11-26
17 NUMBER OF SEQ ID NOS: 14715
18 SOFTWARE: Perl script
19 SEQ ID NO 2380
20 LENGTH: 293
21 TYPE: PRT
22 ORGANISM: Rattus norvegicus
US-10-219-0518-2380

Query Match
Best Local Similarity 88.6% Score 1477; DB 6; Length 293;
Matches 260; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

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Dy 1 MATHESVIFSSASLAVVEYDVLLENFQEPFNANNMLNUNYTKFQIATGSLVIEHA 60
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Db 121 EYNNIPYDWERPNRYLLARCGAVETDTHYFHLHLHKKRYKYHYKHVEFQAPF 180
Oy 181 GKAENYAPLLETLLGCGFVLGCLDQRYVLLWAWVTTLLETIDVHSGYDIPLPLP 240
Db 181 GKAENYAPLLETLLGCGFVLGCLDQRYVLLWAWVTTLLETIDVHSGYDIPLPLP 240
Oy 241 IPTFAGSRHIDRHHNFIQNTASTFTWDRIFGDSQYVAYNKKRKEFKTE 293
Db 241 IPTFAGSRHIDRHHNFIQNTASTFTWDRIFGDSQYVAYNKKRKEFKTE 293
RESULT 6
US-10-537-121-123
Sequence 123, Application US/10537121
Publication No. US20060269917A1
GENERAL INFORMATION:
APPLICANT: diabeaus, Inc.
APPLICANT: Turner, Leah
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Proteins
CURRENT APPLICATION NUMBER: US/10/537,121
FILE REFERENCE: DEK-0449
CURRENT FILING DATE: 2003-06-02
PRIOR FILING DATE: 2003-06-02
PRIOR FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: US 60/431,143
PRIOR FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: US 60/431,206
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 123
LENGTH: 162
ORGANISM: Homo sapiens
US-10-537-121-123
Query Match 55.71; Score 918; DB 6; Length 162;
Best Local Similarity 100.01; Pred. No. 2e-79;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 39 FKKANMYL-----YGNPVLATGMSLNHIEVYVGHAPMIIIDMPSNKKYK 89
Oy 83 IQKDEYTHQKCFVLLPNNKVKYKQKFFTHNKKCFVLLPNNFICLPLGCTGYTTF 135
Db 90 LQDDVPTPQKCKTVYLLSHFTVVELPQISHPICEYGLATHEVFPFHTKIANGI 149
Oy 136 --YLLARCGAVETDTHYFHLHLHKKRYKYHYKHVEFQAPFQACAYAPLETL 193
Db 190 GFLPL-----FDATHNAHRAJHNGPLTHHKKHHSYAPGLAETAPLEVL 200
Oy 194 ILGCGFVLGCLDQRYVLLWAWVTTLLETIDVHSGYDIPLPLPAPLPPAGSR 248
Db 201 ILGCGFVLGCLDQRYVLLWAWVTTLLETIDVHSGYDIPLPLPAPLPPAGSR 260
Oy 249 HHDHNPFIQNTASTFTWDRIFGDSQYVAYNKKRKEFKTE 293
Db 261 HHDHNPFIQNTASTFTWDRIFGDSQYVAYNKKRKEFKTE 303

RESULT 8
US-11-330-403-13559
Sequence 13559, Application US/11330403
Publication No. US2006015962A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53629)B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
NUMBER OF SEQ ID NOS: 19250
SEQ ID NO 13559
LENGTH: 113
TYPE: PRT
ORGANISM: Ustilago maydis 521
US-11-330-403-13559
Query Match 35.41; Score 584; DB 7; Length 113;
Best Local Similarity 39.11; Pred. No. 2.1e-47;
Matches 110; Conservative 48; Mismatches 55; Indels 28; Gaps 4;

Oy 27 NPLOGFNNHNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNY 77
Db 37 NYLERANNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNY 84
Oy 78 MKYKIQKDKPETHNCKWCKVLLPNNFICLPLGCTGYTTFYTHYVDEANRYFY 137

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=110556&ItemName=20070205_152801_us-10-753-267-20.rnphn

Oy 132 MPRVYLLARCGAVETDTHYFHLHLHKKRYKYHYKHVEFQAPFQACAYAPLE 191
Db 1 MPRVYLLARCGAVETDTHYFHLHLHKKRYKYHYKHVEFQAPFQACAYAPLE 60
Oy 192 TLIGTGFGFVLGCLDQRYVLLWAWVTTLLETIDVHSGYDIPLPLPAPLPPAGSR 251
Db 61 TLIGTGFGFVLGCLDQRYVLLWAWVTTLLETIDVHSGYDIPLPLPAPLPPAGSR 120
Oy 252 PHNNFTIGNASTFTWDRIFGDSQYVAYNKKRKEFKTE 293
Db 121 PHNNFTIGNASTFTWDRIFGDSQYVAYNKKRKEFKTE 162
RESULT 7
US-10-449-902-39207
Sequence 39207, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
FILE REFERENCE: MOA-A0205V1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-363870
PRIOR FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 5751
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39207
LENGTH: 317
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-39207
Query Match 36.01; Score 593; DB 6; Length 317;
Best Local Similarity 40.01; Pred. No. 2.9e-48;
Matches 114; Conservative 44; Mismatches 83; Indels 44; Gaps 7;

Oy 33 FKNAM-NYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNN 82
Db 33 FKNAM-NYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNN 82

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=110556&ItemName=20070205_152801_us-10-753-267-20.rnphn

Db 65 MKYKIQKDKPETHNCKWCKVLLPNNFICLPLGCTGYTTFYTHYVDEANRYFY 144
Oy 138 LLARCGAVETDTHYFHLHLHKKRYKYHYKHVEFQAPFQACAYAPLETLIGT 197
Db 145 IANGVFFLPEDATHNAHRAJHNGPLTHHKKHHSYAPGLAETAPLEVLILGN 204
Oy 198 FFGFVLGCLDQRYVLLWAWVTTLLETIDVHSGYDIPLPLPAPLPPAGSRHID 252
Db 205 GTGCGFVLGCLDQRYVLLWAWVTTLLETIDVHSGYDIPLPLPAPLPPAGSR 264
Oy 253 HHDHNPFIQNTASTFTWDRIFGDSQYVAYNKKRKEFKTE 293
Db 265 HHDHNPFIQNTASTFTWDRIFGDSQYVAYNKKRKEFKTE 303

RESULT 9
US-11-330-403-13736
Sequence 13736, Application US/11330403
Publication No. US2006015963A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53629)B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
NUMBER OF SEQ ID NOS: 19250
SEQ ID NO 13736
LENGTH: 305
TYPE: PRT
ORGANISM: GIBBERELLA ZEAE PH-1
US-11-330-403-13736
Query Match 35.31; Score 582; DB 7; Length 305;
Best Local Similarity 43.31; Pred. No. 3.1e-47;
Matches 113; Conservative 46; Mismatches 86; Indels 16; Gaps 7;

Oy 36 ANYNLNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNY 94
Db 41 ANYNLNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNY 97
Oy 95 WCKFVLLPNNFICLPLGCTGYTTFYTHYVDEANRYFYNNYNNYNNYNNYNNY 152
Db 98 WCKFVLLPNNFICLPLGCTGYTTFYTHYVDEANRYFYNNYNNYNNYNNYNNY 154

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=110556&ItemName=20070205_152801_us-10-753-267-20.rnphn

SCORE Search Results Details for Application 10753267 and Search Result 20070205_152755_us-10-753-267-20.rpnbm.

Score from Protein Residue Analysis List SCORE System Overview SCORE EAG Comments / Suggestions

This page gives you Search Results detail for the Application 10753267 and Search Result 20070205_152755_us-10-753-267-20.rpnbm. Back to previous page

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ON protein - protein search, using sw model

Run on: February 6, 2007, 06:01:04 : Search time 182 Seconds
(without alignments)
745.725 Million cell updates/sec

Title: US-10-753-267-20

RefSeq score: 100.00

Sequences: 1 MATHEVSIFSSASLAVVDSLPENLQEPFNHMYNLTNYKFOATWSGLLVHGA 293

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 01
Maximum Match 1001
Listing first 40 summaries

Database :
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2: /BNC_Calerra_31053/pcdata/2/pubseq/US08_PUBCOMB.pep.*
3: /BNC_Calerra_31053/pcdata/2/pubseq/US09_PUBCOMB.pep.*
4: /BNC_Calerra_31053/pcdata/2/pubseq/US10_PUBCOMB.pep.*
5: /BNC_Calerra_31053/pcdata/2/pubseq/US10_PUBCOMB.pep.*

US-09-946-406-6
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ON protein - protein search, using sw model

Run on: February 6, 2007, 06:01:04 : Search time 182 Seconds
(without alignments)
745.725 Million cell updates/sec

Title: US-10-753-267-20

RefSeq score: 100.00

Sequences: 1 MATHEVSIFSSASLAVVDSLPENLQEPFNHMYNLTNYKFOATWSGLLVHGA 293

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 01
Maximum Match 1001
Listing first 40 summaries

Database :
1: /BNC_Calerra_31053/pcdata/2/pubseq/US07_PUBCOMB.pep.*
2: /BNC_Calerra_31053/pcdata/2/pubseq/US08_PUBCOMB.pep.*
3: /BNC_Calerra_31053/pcdata/2/pubseq/US09_PUBCOMB.pep.*
4: /BNC_Calerra_31053/pcdata/2/pubseq/US10_PUBCOMB.pep.*
5: /BNC_Calerra_31053/pcdata/2/pubseq/US10_PUBCOMB.pep.*

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105567&ItemName=20070205_152755_us-10-753-267-20.r... 2/6/07

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ON protein - protein search, using sw model

Run on: February 6, 2007, 06:01:04 : Search time 182 Seconds
(without alignments)
745.725 Million cell updates/sec

Title: US-10-753-267-20

RefSeq score: 100.00

Sequences: 1 MATHEVSIFSSASLAVVDSLPENLQEPFNHMYNLTNYKFOATWSGLLVHGA 293

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 01
Maximum Match 1001
Listing first 40 summaries

Database :
1: /BNC_Calerra_31053/pcdata/2/pubseq/US07_PUBCOMB.pep.*
2: /BNC_Calerra_31053/pcdata/2/pubseq/US08_PUBCOMB.pep.*
3: /BNC_Calerra_31053/pcdata/2/pubseq/US09_PUBCOMB.pep.*
4: /BNC_Calerra_31053/pcdata/2/pubseq/US10_PUBCOMB.pep.*
5: /BNC_Calerra_31053/pcdata/2/pubseq/US10_PUBCOMB.pep.*

US-10-753-267-20
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ON protein - protein search, using sw model

Run on: February 6, 2007, 06:01:04 : Search time 182 Seconds
(without alignments)
745.725 Million cell updates/sec

Title: US-10-753-267-20

RefSeq score: 100.00

Sequences: 1 MATHEVSIFSSASLAVVDSLPENLQEPFNHMYNLTNYKFOATWSGLLVHGA 293

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 01
Maximum Match 1001
Listing first 40 summaries

Database :
1: /BNC_Calerra_31053/pcdata/2/pubseq/US07_PUBCOMB.pep.*
2: /BNC_Calerra_31053/pcdata/2/pubseq/US08_PUBCOMB.pep.*
3: /BNC_Calerra_31053/pcdata/2/pubseq/US09_PUBCOMB.pep.*
4: /BNC_Calerra_31053/pcdata/2/pubseq/US10_PUBCOMB.pep.*
5: /BNC_Calerra_31053/pcdata/2/pubseq/US10_PUBCOMB.pep.*

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105567&ItemName=20070205_152755_us-10-753-267-20.r... 2/6/07

6: /BNC_Calerra_31053/pcdata/2/pubseq/US11_PUBCOMB.pep.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Match	Length	DB ID	Description				
1	1649	100.0	293	3	US-09-946-406-6	Sequence 6, Appl			
2	1649	100.0	293	4	US-10-353-690-4	Sequence 4, Appl			
3	1649	100.0	293	4	US-10-484-978-6	Sequence 6, Appl			
4	1649	100.0	293	5	US-10-753-267-20	Sequence 20, Appl			
5	1649	100.0	293	5	US-10-753-267-20	Sequence 20, Appl			
6	1477	89.6	293	5	US-10-784-004-388	Sequence 368			
7	542.5	32.9	291	4	US-10-425-114-61110	Sequence 61110, A			
8	542.5	32.9	291	4	US-10-425-115-270263	Sequence 270263			
9	541	32.8	318	4	US-10-425-114-42476	Sequence 42476, A			
10	541	32.8	318	4	US-10-425-114-47836	Sequence 47836, A			
11	539.5	32.7	268	4	US-10-437-963-187247	Sequence 187247			
12	539.5	32.7	268	4	US-10-437-963-187247	Sequence 187247			
13	533.5	32.4	294	4	US-10-425-115-270265	Sequence 270265			
14	529.5	32.1	327	4	US-10-128-714-8311	Sequence 8311, A			
15	528	32.0	266	4	US-10-437-963-154358	Sequence 154358			
16	517.5	31.4	271	4	US-10-424-599-246127	Sequence 246127			
17	504.5	30.6	293	4	US-10-437-963-154360	Sequence 154360			
18	503.5	30.5	321	4	US-10-032-585-7322	Sequence 7322, Ap			
19	502.5	30.3	322	4	US-10-032-585-7322	Sequence 7322, Ap			
20	492.5	29.9	323	4	US-10-735-930-6745	Sequence 6745, Ap			
21	482.5	29.3	259	5	US-10-735-930-6745	Sequence 6745, Ap			
22	472.5	28.7	248	4	US-10-259-194A-220	Sequence 220, App			
23	465	28.2	293	4	US-10-128-714-3311	Sequence 3311, Ap			
24	464.5	28.2	284	4	US-10-425-115-270268	Sequence 270268			
25	409	24.8	297	4	US-10-424-599-231951	Sequence 231951			
26	409	24.8	297	5	US-10-439-092-12	Sequence 12, Appl			
27	409	24.8	297	5	US-10-439-092-12	Sequence 12, Appl			
28	397	24.1	299	5	US-10-439-092-7	Sequence 7, Appl			
29	393.5	23.9	298	5	US-10-439-092-7	Sequence 7, Appl			
30	379	23.0	298	5	US-10-439-092-11	Sequence 11, Appl			
31	379	23.0	301	4	US-10-425-115-356023	Sequence 356023			
32	379	23.0	301	5	US-10-439-092-5	Sequence 5, Appl			
33	379	23.0	339	4	US-10-425-114-61805	Sequence 61805, A			
34	379	23.0	335	4	US-10-425-114-60530	Sequence 60530, A			

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105567&ItemName=20070205_152755_us-10-753-267-20.r... 2/6/07

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ON protein - protein search, using sw model

Run on: February 6, 2007, 06:01:04 : Search time 182 Seconds
(without alignments)
745.725 Million cell updates/sec

Title: US-10-753-267-20

RefSeq score: 100.00

Sequences: 1 MATHEVSIFSSASLAVVDSLPENLQEPFNHMYNLTNYKFOATWSGLLVHGA 293

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 01
Maximum Match 1001
Listing first 40 summaries

Database :
1: /BNC_Calerra_31053/pcdata/2/pubseq/US07_PUBCOMB.pep.*
2: /BNC_Calerra_31053/pcdata/2/pubseq/US08_PUBCOMB.pep.*
3: /BNC_Calerra_31053/pcdata/2/pubseq/US09_PUBCOMB.pep.*
4: /BNC_Calerra_31053/pcdata/2/pubseq/US10_PUBCOMB.pep.*
5: /BNC_Calerra_31053/pcdata/2/pubseq/US10_PUBCOMB.pep.*

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ON protein - protein search, using sw model

Run on: February 6, 2007, 06:01:04 : Search time 182 Seconds
(without alignments)
745.725 Million cell updates/sec

Title: US-10-753-267-20

RefSeq score: 100.00

Sequences: 1 MATHEVSIFSSASLAVVDSLPENLQEPFNHMYNLTNYKFOATWSGLLVHGA 293

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 01
Maximum Match 1001
Listing first 40 summaries

Database :
1: /BNC_Calerra_31053/pcdata/2/pubseq/US07_PUBCOMB.pep.*
2: /BNC_Calerra_31053/pcdata/2/pubseq/US08_PUBCOMB.pep.*
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4: /BNC_Calerra_31053/pcdata/2/pubseq/US10_PUBCOMB.pep.*
5: /BNC_Calerra_31053/pcdata/2/pubseq/US10_PUBCOMB.pep.*

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105567&ItemName=20070205_152755_us-10-753-267-20.r... 2/6/07

1 PRIOR APPLICATION NUMBER: 60/351,224
2 PRIOR FILING DATE: 2002-02-01
3 PRIOR APPLICATION NUMBER: 60/364,529
4 PRIOR FILING DATE: 2002-03-15
5 PRIOR APPLICATION NUMBER: 60/371,861
6 PRIOR FILING DATE: 2002-04-19
7 PRIOR APPLICATION NUMBER: 60/376,287
8 PRIOR FILING DATE: 2002-05-02
9 PRIOR APPLICATION NUMBER: 60/388,080
10 PRIOR FILING DATE: 2002-06-12
11 PRIOR APPLICATION NUMBER: 60/390,971
12 PRIOR FILING DATE: 2002-06-24
13 PRIOR APPLICATION NUMBER: 60/394,130
14 PRIOR FILING DATE: 2002-07-03
15 PRIOR APPLICATION NUMBER: 60/394,797
16 PRIOR FILING DATE: 2002-07-03
17 PRIOR APPLICATION NUMBER: 60/404,904
18 PRIOR FILING DATE: 2002-08-21
19 PRIOR APPLICATION NUMBER: 60/405,450
20 PRIOR FILING DATE: 2002-08-23
21 Remaining Prior Application data removed - See File Wrapper or PALM.
22 NUMBER OF SEQ ID NOS: 126
23 SOFTWARE: FastSeq for Windows Version 4.0
24 SEQ ID NO: 1
25 LENGTH: 293
26 TYPE: PRT
27 ORGANISM: Homo Sapiens
28 US-10-353-690-4

Query Match 100.0%; Score 1649; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 6.8e-161;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MATNESVIFSSASLAVEYDLSLPENLPQEPFNANNMLNNYTKFOIATGSLIVHEA 60
Db 1 MATNESVIFSSASLAVEYDLSLPENLPQEPFNANNMLNNYTKFOIATGSLIVHEA 60
Oy 61 LVYFCLPGPLPQFPIPMKKYKIDONKPEHMKCFVLLPNNFCIOLPLIGCTYPT 120
Db 61 LVYFCLPGPLPQFPIPMKKYKIDONKPEHMKCFVLLPNNFCIOLPLIGCTYPT 120
Oy 121 EYFNPIYDMENPRMYTLARCGCAVIEDTNYFJRLHLHNRKYIKYHKNHFEQAPF 180
Db 121 EYFNPIYDMENPRMYTLARCGCAVIEDTNYFJRLHLHNRKYIKYHKNHFEQAPF 180

http://es/ScoreAccessWeb/GdlItem.action?AppId=10753267&seqId=1105367&ItemName=20070205_152755_us-10-753-267-20.rnphm 2/8/07

Oy 121 EYFNPIYDMENPRMYTLARCGCAVIEDTNYFJRLHLHNRKYIKYHKNHFEQAPF 180
Db 121 EYFNPIYDMENPRMYTLARCGCAVIEDTNYFJRLHLHNRKYIKYHKNHFEQAPF 180
Oy 181 GHEAYANPLETLLGTGFFIGVLLCDRVILLMAWVTIRLLETIDVHSGYDIFLPLNL 240
Db 181 GHEAYANPLETLLGTGFFIGVLLCDRVILLMAWVTIRLLETIDVHSGYDIFLPLNL 240
Oy 241 IFTFAGSHDHPHNNFTIGNVASTFTWDRIFGTDGQYWAYNEKKKFEKTE 293
Db 241 IFTFAGSHDHPHNNFTIGNVASTFTWDRIFGTDGQYWAYNEKKKFEKTE 293

RESULT 4
US-10-753-267-20
2 Publication No. US20030037946A1
3 GENERAL INFORMATION:
4 APPLICANT: Millennium Pharmaceuticals, Inc.
5 APPLICANT: Steglino, Nancy E.
6 APPLICANT: Acton, Susan L.
7 APPLICANT: Acton, Susan L.
8 APPLICANT: Rodriguez-Wray, Amelie
9 APPLICANT: Rodriguez-Wray, Amelie
10 APPLICANT: Tomlinson, James E.
11 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
12 TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
13 TITLE OF INVENTION: 10639, 9235, 21668, 31794, 2210, 6169, 10102, 21061, 17662,
14 TITLE OF INVENTION: 3533, 9442, 9123, 12788, 1779, 65552, 1241, 21436, 33770,
15 TITLE OF INVENTION: 9380, 2589654, 33566, 44193, 32612, 10671, 261,
16 TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 89931, 955,
17 TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
18 TITLE OF INVENTION: 42028, 112091, 13866, 13942, 1673, 54946 OR 2419
19 FILE REFERENCE: MF03-003DIPNOMHJM
20 CURRENT FILING DATE: 2004-01-08
21 PRIOR APPLICATION NUMBER: US 60/439,683
22 PRIOR FILING DATE: 2003-01-13
23 PRIOR APPLICATION NUMBER: US 60/445,216
24 PRIOR FILING DATE: 2003-02-05
25 PRIOR APPLICATION NUMBER: US 60/448,036
26 PRIOR FILING DATE: 2003-02-18

http://es/ScoreAccessWeb/GdlItem.action?AppId=10753267&seqId=1105367&ItemName=20070205_152755_us-10-753-267-20.rnphm 2/8/07

Oy 181 GHEAYANPLETLLGTGFFIGVLLCDRVILLMAWVTIRLLETIDVHSGYDIFLPLNL 240
Db 181 GHEAYANPLETLLGTGFFIGVLLCDRVILLMAWVTIRLLETIDVHSGYDIFLPLNL 240
Oy 241 IFTFAGSHDHPHNNFTIGNVASTFTWDRIFGTDGQYWAYNEKKKFEKTE 293
Db 241 IFTFAGSHDHPHNNFTIGNVASTFTWDRIFGTDGQYWAYNEKKKFEKTE 293

RESULT 3
US-10-684-978-6
2 Sequence 6; Application US/10684978
3 Publication No. US20040166485A1
4 GENERAL INFORMATION:
5 APPLICANT: Herman, Gail E.
6 APPLICANT: Herman, Gail E.
7 APPLICANT: Granger, Deborah K.
8 APPLICANT: Granger, Deborah K.
9 TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO CHOLESTEROL
10 TITLE OF INVENTION: BIOSYNTHESIS ENZYMES
11 FILE REFERENCE: 28335/16435
12 CURRENT APPLICATION NUMBER: US/10/684,978
13 CURRENT FILING DATE: 2003-10-14
14 PRIOR APPLICATION NUMBER: US/09/588,976
15 PRIOR FILING DATE: 2003-06-01
16 PRIOR APPLICATION NUMBER: 60/137,020
17 PRIOR FILING DATE: 1999-06-01
18 NUMBER OF SEQ ID NOS: 28
19 SOFTWARE: PatentIn Ver. 2.0
20 SEQ ID NO: 6
21 LENGTH: 293
22 TYPE: PRT
23 ORGANISM: Homo sapiens
24 US-10-684-978-6

Query Match 100.0%; Score 1649; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 6.8e-161;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MATNESVIFSSASLAVEYDLSLPENLPQEPFNANNMLNNYTKFOIATGSLIVHEA 60
Db 1 MATNESVIFSSASLAVEYDLSLPENLPQEPFNANNMLNNYTKFOIATGSLIVHEA 60
Oy 61 LVYFCLPGPLPQFPIPMKKYKIDONKPEHMKCFVLLPNNFCIOLPLIGCTYPT 120
Db 61 LVYFCLPGPLPQFPIPMKKYKIDONKPEHMKCFVLLPNNFCIOLPLIGCTYPT 120
Oy 121 EYFNPIYDMENPRMYTLARCGCAVIEDTNYFJRLHLHNRKYIKYHKNHFEQAPF 180
Db 121 EYFNPIYDMENPRMYTLARCGCAVIEDTNYFJRLHLHNRKYIKYHKNHFEQAPF 180

http://es/ScoreAccessWeb/GdlItem.action?AppId=10753267&seqId=1105367&ItemName=20070205_152755_us-10-753-267-20.rnphm 2/8/07

2 PRIOR APPLICATION NUMBER: US 60/454,189
3 PRIOR FILING DATE: 2003-03-12
4 PRIOR APPLICATION NUMBER: US 60/457,541
5 PRIOR FILING DATE: 2003-03-25
6 PRIOR APPLICATION NUMBER: US 60/466,411
7 PRIOR FILING DATE: 2003-04-29
8 PRIOR APPLICATION NUMBER: US 60/469,041
9 PRIOR FILING DATE: 2003-05-08
10 PRIOR APPLICATION NUMBER: US 60/477,414
11 PRIOR FILING DATE: 2003-06-10
12 PRIOR APPLICATION NUMBER: US 60/478,560
13 PRIOR FILING DATE: 2003-06-13
14 PRIOR APPLICATION NUMBER: US 60/485,772
15 PRIOR FILING DATE: 2003-07-24
16 Remaining Prior Application data removed - See File Wrapper or PALM.
17 NUMBER OF SEQ ID NOS: 130
18 SOFTWARE: PatentIn Ver. 2.0
19 SEQ ID NO: 20
20 LENGTH: 293
21 TYPE: PRT
22 ORGANISM: Homo Sapiens
23 US-10-753-267-20

Query Match 100.0%; Score 1649; DB 5; Length 293;
Best Local Similarity 100.0%; Pred. No. 6.8e-161;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MATNESVIFSSASLAVEYDLSLPENLPQEPFNANNMLNNYTKFOIATGSLIVHEA 60
Oy 61 LVYFCLPGPLPQFPIPMKKYKIDONKPEHMKCFVLLPNNFCIOLPLIGCTYPT 120
Db 61 LVYFCLPGPLPQFPIPMKKYKIDONKPEHMKCFVLLPNNFCIOLPLIGCTYPT 120
Oy 121 EYFNPIYDMENPRMYTLARCGCAVIEDTNYFJRLHLHNRKYIKYHKNHFEQAPF 180
Db 121 EYFNPIYDMENPRMYTLARCGCAVIEDTNYFJRLHLHNRKYIKYHKNHFEQAPF 180
Oy 181 GHEAYANPLETLLGTGFFIGVLLCDRVILLMAWVTIRLLETIDVHSGYDIFLPLNL 240
Db 181 GHEAYANPLETLLGTGFFIGVLLCDRVILLMAWVTIRLLETIDVHSGYDIFLPLNL 240
Oy 241 IFTFAGSHDHPHNNFTIGNVASTFTWDRIFGTDGQYWAYNEKKKFEKTE 293
Db 241 IFTFAGSHDHPHNNFTIGNVASTFTWDRIFGTDGQYWAYNEKKKFEKTE 293

http://es/ScoreAccessWeb/GdlItem.action?AppId=10753267&seqId=1105367&ItemName=20070205_152755_us-10-753-267-20.rnphm 2/8/07

Db 241 1PFTAGSRHHDFHNNFTIGNYASTFTWDRILFOTDSQYWAYNEKKKFEKTE 293

RESULT 5

US-10-784-004-689

/ Sequence 689, Application US/10784004

/ Publication No. US20060084066A1

/ GENERAL INFORMATION:

/ APPLICANT: Biogen Idec

/ TITLE OF INVENTION: Surrogate Markers of Pain

/ FILING DATE: 2004-02-20

/ CURRENT APPLICATION NUMBER: US/10/784,004

/ CURRENT FILING DATE: 2004-02-20

/ NUMBER OF SEQ ID NOS: 1251

/ SOFTWARE: PatentIn version 3.2

/ SEQ ID NO 689

/ LENGTH: 293

/ TYPE: PRT

/ ORGANISM: human

US-10-784-004-689

Query Match 100.0%; Score 1649; DB 5; Length 293;

Best Local Similarity 100.0%; Pred. No. 6.8e-161; Mismatches 0; Indels 0; Gaps 0;

Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NATHESVIFSSASLAVYDVSLLPENLPQEPFKNNMUNNYTFQIATGSLIVHEA 60

Db 1 NATHESVIFSSASLAVYDVSLLPENLPQEPFKNNMUNNYTFQIATGSLIVHEA 60

Oy 61 LYVFLCPLGFLPOTIPNNKYKIQOKETEMHOKKCFVLLPHNFCIOLPLICGTYTFF 120

Db 61 LYVFLCPLGFLPOTIPNNKYKIQOKETEMHOKKCFVLLPHNFCIOLPLICGTYTFF 120

Oy 121 EYFNIPYDMENRMYTLLAKGCGAVIEDRWYFJHRLHNNRYKYIKYHVKHVEFQAPF 180

Db 121 EYFNIPYDMENRMYTLLAKGCGAVIEDRWYFJHRLHNNRYKYIKYHVKHVEFQAPF 180

Oy 131 EYFNIPYDMENRMYTLLAKGCGAVIEDRWYFJHRLHNNRYKYIKYHVKHVEFQAPF 180

Db 131 EYFNIPYDMENRMYTLLAKGCGAVIEDRWYFJHRLHNNRYKYIKYHVKHVEFQAPF 180

Oy 181 GREAYANPLETLILGTFPGFIVGLCDHVLNMMVYTRILLETIDVHSGDTIFLPLNL 240

Db 181 GREAYANPLETLILGTFPGFIVGLCDHVLNMMVYTRILLETIDVHSGDTIFLPLNL 240

Oy 241 1PFTAGSRHHDFHNNFTIGNYASTFTWDRILFOTDSQYWAYNEKKKFEKTE 293

Db 241 1PFTAGSRHHDFHNNFTIGNYASTFTWDRILFOTDSQYWAYNEKKKFEKTE 293

RESULT 7

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105567&ItemName=20070205_152755_us-10-753-267-20.r... 2/8/07

US-10-425-114-61110

/ Sequence 6110, Application US/10425114

/ Publication No. US20040034088A1

/ GENERAL INFORMATION:

/ APPLICANT: Liu, Jingdong

/ APPLICANT: Zhou, Yihua

/ APPLICANT: Kowalc, David K.

/ APPLICANT: Screen, Steven E

/ APPLICANT: Tobazaki, Jack E

/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

/ CURRENT APPLICATION NUMBER: US/10/425,114

/ CURRENT FILING DATE: 2003-04-28

/ NUMBER OF SEQ ID NOS: 73128

/ SEQ ID NO 6110

/ LENGTH: 291

/ TYPE: PRT

/ ORGANISM: Zea mays

/ FEATURE:

/ OTHER INFORMATION: Clone ID: LB1332-023-HB_FLI.pep

US-10-425-114-61110

Query Match 32.9%; Score 542.5; DB 4; Length 291;

Best Local Similarity 38.6%; Pred. No. 4.9e-47; Mismatches 108; Conservative 49; Mismatches 98; Indels 25; Gaps 6;

Oy 27 NPLQEP-----FNANNMUNNYTFQIATGSLIVHEALYFLCFLGFLQFIPQM 78

Db 17 SPPLSAVYLSLAIQANOLLNPTFQIATGSLIVHEALYFLCFLGFLQFIPQM 78

Oy 79 KYVYQKPKETEMHOKKCFVLLPHNFCIOLPLICGTYTFFYF---HFTYDMENR 134

Db 71 AKYVQK-KSTSAVQKROVLRLLVYQVNLPMVYSPAKFKNGLSLSP-----LPH 130

Oy 135 WYFLARCGCAVIEDRWYFJHRLHNNRYKYIKYHVKHVEFQAPFQMEAYANPLETLI 194

Db 131 MSVVSVQVLYFVLEDFIFMGHRAUKTMYKXHVHVEYATVPGLTSEYANPAELF 190

Oy 195 LGTGTGFGIVGLCDHVLNMMVYTRILLETIDVHSGDTIFLPLNL1PFTAGSRHHDFH 254

Db 191 LGFATVCGALTPHLLTNMUNYLVLETVHSGDTIFLPLNL1PFTAGSRHHDFH 250

Oy 255 NMFY---GNYASTFTWDRILFOTDSQYWAYNEKKKFEK 291

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105567&ItemName=20070205_152755_us-10-753-267-20.r... 2/8/07

RESULT 6

US-10-784-004-368

/ Sequence 368, Application US/10784004

/ Publication No. US20060084066A1

/ GENERAL INFORMATION:

/ APPLICANT: Biogen Idec

/ TITLE OF INVENTION: Surrogate Markers of Pain

/ FILING DATE: 2004-02-20

/ CURRENT APPLICATION NUMBER: US/10/784,004

/ CURRENT FILING DATE: 2004-02-20

/ NUMBER OF SEQ ID NOS: 1251

/ SOFTWARE: PatentIn version 3.2

/ SEQ ID NO 368

/ LENGTH: 293

/ TYPE: PRT

/ ORGANISM: rat

US-10-784-004-368

Query Match 89.6%; Score 1477; DB 5; Length 293;

Best Local Similarity 88.7%; Pred. No. 3.4e-143; Mismatches 260; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Oy 1 NATHESVIFSSASLAVYDVSLLPENLPQEPFKNNMUNNYTFQIATGSLIVHEA 60

Db 1 NATHESVIFSSASLAVYDVSLLPENLPQEPFKNNMUNNYTFQIATGSLIVHEA 60

Oy 61 LYVFLCPLGFLPOTIPNNKYKIQOKETEMHOKKCFVLLPHNFCIOLPLICGTYTFF 120

Db 61 LYVFLCPLGFLPOTIPNNKYKIQOKETEMHOKKCFVLLPHNFCIOLPLICGTYTFF 120

Oy 121 EYFNIPYDMENRMYTLLAKGCGAVIEDRWYFJHRLHNNRYKYIKYHVKHVEFQAPF 180

Db 121 EYFNIPYDMENRMYTLLAKGCGAVIEDRWYFJHRLHNNRYKYIKYHVKHVEFQAPF 180

Oy 131 EYFNIPYDMENRMYTLLAKGCGAVIEDRWYFJHRLHNNRYKYIKYHVKHVEFQAPF 180

Db 131 EYFNIPYDMENRMYTLLAKGCGAVIEDRWYFJHRLHNNRYKYIKYHVKHVEFQAPF 180

Oy 181 GREAYANPLETLILGTFPGFIVGLCDHVLNMMVYTRILLETIDVHSGDTIFLPLNL 240

Db 181 GREAYANPLETLILGTFPGFIVGLCDHVLNMMVYTRILLETIDVHSGDTIFLPLNL 240

Oy 241 1PFTAGSRHHDFHNNFTIGNYASTFTWDRILFOTDSQYWAYNEKKKFEKTE 293

Db 241 1PFTAGSRHHDFHNNFTIGNYASTFTWDRILFOTDSQYWAYNEKKKFEKTE 293

RESULT 7

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105567&ItemName=20070205_152755_us-10-753-267-20.r... 2/8/07

Db 251 RVLTYSQYASTFTWDRILFOTDSQYWAYNEKKKFEKTE 286

US-10-425-115-270263

/ Sequence 270263, Application US/10425115

/ Publication No. US20040214272A1

/ GENERAL INFORMATION:

/ APPLICANT: Kowalc, David K.

/ APPLICANT: Zhou, Yihua

/ APPLICANT: Screen, Steven E

/ APPLICANT: Tobazaki, Jack E

/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

/ TITLE OF INVENTION: Plants

/ FILE REFERENCE: 38-2153223B

/ CURRENT APPLICATION NUMBER: US/10/425,115

/ CURRENT FILING DATE: 2003-04-28

/ NUMBER OF SEQ ID NOS: 169326

/ SEQ ID NO 270263

/ LENGTH: 291

/ TYPE: PRT

/ ORGANISM: Zea mays

/ FEATURE:

/ OTHER INFORMATION: Clone ID: HRT4577_176077C-1.pep

US-10-425-115-270263

Query Match 32.9%; Score 542.5; DB 4; Length 291;

Best Local Similarity 38.6%; Pred. No. 4.9e-47; Mismatches 108; Conservative 49; Mismatches 98; Indels 25; Gaps 6;

Oy 27 NPLQEP-----FNANNMUNNYTFQIATGSLIVHEALYFLCFLGFLQFIPQM 78

Db 17 SPPLSAVYLSLAIQANOLLNPTFQIATGSLIVHEALYFLCFLGFLQFIPQM 78

Oy 79 KYVYQKPKETEMHOKKCFVLLPHNFCIOLPLICGTYTFFYF---HFTYDMENR 134

Db 71 AKYVQK-KSTSAVQKROVLRLLVYQVNLPMVYSPAKFKNGLSLSP-----LPH 130

Oy 135 WYFLARCGCAVIEDRWYFJHRLHNNRYKYIKYHVKHVEFQAPFQMEAYANPLETLI 194

Db 131 MSVVSVQVLYFVLEDFIFMGHRAUKTMYKXHVHVEYATVPGLTSEYANPAELF 190

Oy 195 LGTGTGFGIVGLCDHVLNMMVYTRILLETIDVHSGDTIFLPLNL1PFTAGSRHHDFH 254

Db 191 LGFATVCGALTPHLLTNMUNYLVLETVHSGDTIFLPLNL1PFTAGSRHHDFH 250

Oy 255 NMFY---GNYASTFTWDRILFOTDSQYWAYNEKKKFEK 291

Db 191 LQATVAGPALTGPHLTATLAKVAVLETVDAISCHTFPWSJSHVLEPLTGGSDPHDHR 250
Oy 255 MWFI---GNYASTFWMDRIFGTDSOTYNAERKKFEK 291
Db 251 RVLTSGNYASTFVMDLFGTDKY---RKATTEEK 286

RESULT 9
US-10-425-114-42476
? Sequence 42476, Application US/10425114
? Publication No. US2004003488A1
? GENERAL INFORMATION:
? APPLICANT: Liu, Jingdong
? APPLICANT: Zhou, Yihua
? APPLICANT: Kovacic, David K.
? APPLICANT: Screen, Steven E
? APPLICANT: Tabaka, Jack E
? APPLICANT: Cao, Yomei
? APPLICANT: Cao, Yomei
? TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
? FILE REFERENCE: 38-2153313B
? CURRENT APPLICATION NUMBER: US/10/425,114
? NUMBER OF SEQ ID NOS: 20486
? SEQ ID NO 187247
? LENGTH: 268
? TYPE: PRT
? ORGANISM: Zea mays
? FEATURE:
? OTHER INFORMATION: Clone ID: 700235424_FLI.pep
US-10-425-114-42476

Query Match 32.84; Score 541; DB 4; Length 318;
Best Local Similarity 37.54; Pred. No. 7.8e-47;
Matches 110; Conservative 53; Mismatches 98; Indels 32; Gaps 7;

Oy 6 SVSIFSSALVAYSDSLPENLOEPFKHANNMUNYTFQATWGSIVHEALVYLF 65
Db 46 S1SLTAAWNSA--1DS-----AQGLIANFTFQATVYTLRLHYTFLLS 90

Oy 66 CLGFLGFTFPMKKYIKOKPTEWQKFKVLLFNHPCIDGLCGTGYTFYF-- 123
Db 91 GLPLFLERGLCAKYIKOK-KSHTATYQRCVGLLHVVCNVPMTSPYAFKMG 149

Oy 124 --NIPYDWMNPRVFLARCGAVIEDPRHYFLRLHKKRYIKVHKVHGFQAPG 181

Db 150 RSLP-----LPHMSVVSQVLPYVLEDFITFQGBALHTKMLYKRVHVEYATPG 204
Oy 182 MEATYAHPLLETIGTGFFGIVLCORVILLMMWMTIRLLETIDVHSGYDIPLMPLMI 241
Db 205 LTSEYAHPLILFGATYVVGALTPGPHLPLMLVLETVHSGYHGFHFPSPNPL 264
Oy 242 PFYAGSRHGHFHMNT---GNYASTFWMDRIFGTDSOTYNAERKKFEK 291
Db 265 PLYGSDPHDHRVLTSGNYASTFVMDLFGTDKY---RKATTEEK 313

RESULT 10
US-10-425-114-47836
? Sequence 47836, Application US/10425114
? Publication No. US2004003488A1
? GENERAL INFORMATION:
? APPLICANT: Liu, Jingdong
? APPLICANT: Zhou, Yihua
? APPLICANT: Kovacic, David K.
? APPLICANT: Screen, Steven E
? APPLICANT: Tabaka, Jack E
? APPLICANT: Cao, Yomei
? APPLICANT: Cao, Yomei
? TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
? FILE REFERENCE: 38-2153313B
? CURRENT APPLICATION NUMBER: US/10/425,114
? NUMBER OF SEQ ID NOS: 20486
? SEQ ID NO 17836
? LENGTH: 318
? TYPE: PRT
? ORGANISM: Zea mays
? FEATURE:
? OTHER INFORMATION: Clone ID: 700263728_FLI.pep
US-10-425-114-47836

Query Match 32.88; Score 541; DB 4; Length 318;
Best Local Similarity 37.54; Pred. No. 7.8e-47;
Matches 110; Conservative 53; Mismatches 98; Indels 32; Gaps 7;

Oy 6 SVSIFSSALVAYSDSLPENLOEPFKHANNMUNYTFQATWGSIVHEALVYLF 65
Db 46 S1SLTAAWNSA--1DS-----AQGLIANFTFQATVYTLRLHYTFLLS 90

Oy 66 CLGFLGFTFPMKKYIKOKPTEWQKFKVLLFNHPCIDGLCGTGYTFYF-- 123
Db 91 GLPLFLERGLCAKYIKOK-KSHTATYQRCVGLLHVVCNVPMTSPYAFKMG 149

Oy 124 --NIPYDWMNPRVFLARCGAVIEDPRHYFLRLHKKRYIKVHKVHGFQAPG 181
Db 150 RSLP-----LPHMSVVSQVLPYVLEDFITFQGBALHTKMLYKRVHVEYATPG 204

Oy 182 MEATYAHPLLETIGTGFFGIVLCORVILLMMWMTIRLLETIDVHSGYDIPLMPLMI 241
Db 205 LTSEYAHPLILFGATYVVGALTPGPHLPLMLVLETVHSGYHGFHFPSPNPL 264

Oy 242 PFYAGSRHGHFHMNT---GNYASTFWMDRIFGTDSOTYNAERKKFEK 291
Db 265 PLYGSDPHDHRVLTSGNYASTFVMDLFGTDKY---RKATTEEK 313

RESULT 11
US-10-437-963-187247
? Sequence 187247, Application US/10437963
? Publication No. US2004012349A1
? GENERAL INFORMATION:
? APPLICANT: La Rosa, Thomas J.
? APPLICANT: Kovacic, David K.
? APPLICANT: Cao, Yomei
? APPLICANT: Wu, Wei
? APPLICANT: Boutharov, Audrey A.
? APPLICANT: Balazuk, Brad
? APPLICANT: Li, Ping
? TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
? FILE REFERENCE: 38-2153213B
? CURRENT APPLICATION NUMBER: US/10/437,963
? CURRENT FILING DATE: 2003-05-18
? NUMBER OF SEQ ID NOS: 204866
? SEQ ID NO 187247
? LENGTH: 268
? TYPE: PRT
? ORGANISM: Oryza sativa
? FEATURE:
? OTHER INFORMATION: Clone ID: PAT_MPT4530_3396C-1.pep
US-10-437-963-187247

Query Match 32.74; Score 539.5; DB 4; Length 268;

Best Local Similarity 38.53; Pred. No. 9e-47;
Matches 102; Conservative 54; Mismatches 92; Indels 17; Gaps 5;

Oy 34 KXANNMUNYTFQATWGSIVHEALVYLCPLGFLGFTFPMKKYIKOKPTEWEN 93
Db 8 ESAMEYLITFSEFQASIGTGLHVSIVFLGSLPLPERGLGFSKYIKOK-KSHTPDY 66

Oy 94 QWCKFVLPHPICIDGLCGTGYTFYF---NIPYDWMNPRVFLARCGAVIE 149
Db 67 QRCVRLVLCVLCPLTILSYTFYFNGSLTP-----LPHMTVVSQVLPFVLE 121

Oy 150 DTHIVYFLRLHKKRYIKVHKVHGFQAPGAEYAHPLLETIGTGFFGIVLCOM 209
Db 122 DFTFQGBALHTKMLYKRVHVEYATFPGTSEYAHPLLETIGATVAGTALGPH 181

Oy 210 VILLMMWMTIRLLETIDVHSGYDIPLMPLLETIFPKASRHDPHNMNT---GHVASTF 266
Db 182 LPTLVKVVLETVHSGYHGFHFPSPNPLYGGAFFDHRVLTSGNYSTFTI 241

Oy 267 WMDRIFGTDSOTYNAERKKFEK 291
Db 242 YMDLFGTDKY---RKATTEEK 282

RESULT 12
US-10-767-701-45894
? Sequence 45894, Application US/10767701
? Publication No. US2004017268A1
? GENERAL INFORMATION:
? APPLICANT: Kovacic, David K.
? APPLICANT: Zhou, Yihua
? APPLICANT: Cao, Yomei
? APPLICANT: Cao, Yomei
? TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
? FILE REFERENCE: 38-2153313B
? CURRENT APPLICATION NUMBER: US/10/767,701
? CURRENT FILING DATE: 2004-01-29
? NUMBER OF SEQ ID NOS: 63128
? SEQ ID NO 45894
? LENGTH: 268
? TYPE: PRT
? ORGANISM: Sorghum bicolor
? FEATURE:
? OTHER INFORMATION: Clone ID: SORBI-28MA703-C1622_1.p.p
US-10-767-701-45894

OY 211 ILWAVTIRLETDVHGVDSPLUPJLIPPTIAGSRHDPKUNVI---GNVASTFW 267
DB 182 PTLUNKLVLETVKAGVNFWSRFLYGGSDTHYHRVLTSHGVASTFW 241
OY 268 MDRIFGTDSQY---WYNKRKK 287
DB 242 MDVLFCTMDYKAKAIBKDKR 264

Search completed: February 6, 2007, 06:06:15
Job time : 194 secs

SCORE Search Results Details for Application 10753267 and Search Result 20070205_152740_us-10-753-267-20.rai.

ScoreMatchPair RetrievalApplicationLink SCORESystemOverview SCOREFAQ CommentsSuggestions

This page gives you Search Results detail for the Application 10753267 and Search Result 20070205_152740_us-10-753-267-20.rai.

Back

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OM protein - protein search, using sw model

Run on: February 6, 2007, 05:48:49 / Search time 51 Seconds
(Without alignments)
502.872 Million cell updates/aac

Title: US-10-753-267-20
Perfect score: 1649
Sequence: 1 MATHESVSIFFSASLAVYDLSPEPFLPNNYKFNATYKFIQTATGSLIVHEALYFLF 65

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues
Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum Match 1001
Listing first 45 summaries

Post-processing: Minimum Match 01
Maximum Match 1001
Listing first 45 summaries

Database : Issued Patents AA*
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3: /BPC_Celera_31D33/ptoddata/2/1aa/7 COMB.pep.*
4: /BPC_Celera_31D33/ptoddata/2/1aa/8 COMB.pep.*
5: /BPC_Celera_31D33/ptoddata/2/1aa/9 COMB.pep.*

US-09-513-999C-5238
Sequence 5238, Appl
Sequence 20, Appl
Sequence 24, Appl
Sequence 17951, A
Sequence 17950, A
Sequence 6, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 7967, Ap
Sequence 22, Appl
Sequence 8142, Ap
Sequence 8146, A
Sequence 17952, A
Sequence 32, Appl
Sequence 30, Appl
Sequence 26, Appl
Sequence 24, Appl
Sequence 33, Appl
Sequence 32044, A
Sequence 42661, A
Sequence 20672, A
Sequence 17952, A
Sequence 10, Appl
Sequence 28, Appl
Sequence 24, Appl

Sequence 29468, A
Sequence 6, Appl
Sequence 5, Appl
Sequence 18, Appl
Sequence 14, Appl
Sequence 13071, A
Sequence 3032, A
Sequence 10330, A
Sequence 16, Appl
Sequence 16089, A
Sequence 562, App

US-09-513-999C-5238
Sequence 5238, Appl
Sequence 20, Appl
Sequence 24, Appl
Sequence 17951, A
Sequence 17950, A
Sequence 6, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 7967, Ap
Sequence 22, Appl
Sequence 8142, Ap
Sequence 8146, A
Sequence 17952, A
Sequence 32, Appl
Sequence 30, Appl
Sequence 26, Appl
Sequence 24, Appl
Sequence 33, Appl
Sequence 32044, A
Sequence 42661, A
Sequence 20672, A
Sequence 17952, A
Sequence 10, Appl
Sequence 28, Appl
Sequence 24, Appl

Sequence 29468, A
Sequence 6, Appl
Sequence 5, Appl
Sequence 18, Appl
Sequence 14, Appl
Sequence 13071, A
Sequence 3032, A
Sequence 10330, A
Sequence 16, Appl
Sequence 16089, A
Sequence 562, App

ALIGNMENTS

RESULT 1
US-09-513-999C-5238
Sequence 5238, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: DuPont, J.B.
APPLICANT: Glaxo, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATENT NO. 6783961
FILE REFERENCE: 59,052,REG
CURRENT APPLICATION NUMBER: US/09/513,999C
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 60/122,487
NUMBER OF SEQ ID NOS: 16681
SOFTWARE: Patent-pm
SEQ ID NO 5238
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 75
OTHER INFORMATION: xaa=ile or Met
US-09-513-999C-5238
Query Match 38.0%; Score 627; DB 2; Length 115;

Best Local Similarity 99.1%; Pred. No. 1,3e-62;
Matches 114; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MATHESVSIFFSASLAVYDLSPEPFLPNNYKFNATYKFIQTATGSLIVHEA 60
Db 1 MATHESVSIFFSASLAVYDLSPEPFLPNNYKFNATYKFIQTATGSLIVHEA 60
Qy 61 LVFLFCPLGFLPFPYKPKYKIQKFKFENKFKFVLLPNNFCIPLICG 115
Db 61 LVFLFCPLGFLPFPYKPKYKIQKFKFENKFKFVLLPNNFCIPLICG 115
RESULT 2
US-09-513-999C-5238
Sequence 20, Application US/09439554
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Rafalski, Jan Antoni
APPLICANT: Odell, Joan T.
APPLICANT: Sakai, Hajime
APPLICANT: Kinney, Anthony J.
APPLICANT: Kameron, Oshay O.
TITLE OF INVENTION: BETA-GLUCOSIDASES
FILE REFERENCE: 88114 US NA
CURRENT APPLICATION NUMBER: US/09/439,554
CURRENT FILING DATE: 1999-11-12
EARLIER APPLICATION NUMBER: 60/108,351
PRIOR FILING DATE: 1998-No. 647973member-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 20
LENGTH: 291
TYPE: PRT
ORGANISM: Zea mays
US-09-439-554-20
Query Match 32.81%; Score 541; DB 2; Length 291;
Best Local Similarity 37.5%; Pred. No. 2.9e-52;
Matches 110; Conservative 53; Mismatches 98; Indels 32; Gaps 7;
Qy 6 SVSIFSSASLAVYDLSPEPFLPNNYKFNATYKFIQTATGSLIVHEALYFLF 65
Db 19 SISLTHAHPAA--DS-----AVOLLIAFTPEPLATYVTFLLHETVFLS 63

Query Match 17.1k; Score 281.5; DB 2; Length 272;
Best Local Similarity 28.5k; Pred. No. 3.3e-23;
Matches 72; Conservative 34; Mismatches 104; Indels 43; Gaps 7;
Oy 52 WGSIVHEAL-----YPLCLP-----GFLPQIPYMKYKIQNDPTEW 93
Db 24 WHLRSEALLOSFFVFIITTYGCLPVPVLDICSWVALRYKHDPSPSAO 83
Oy 94 OKCFVLLPHFICQPLICGTYTYTEYFNIPYMERHNPVYLLARCPCGCAVED 151
Db 84 LLPCGLGTYVHLVFPVTL--LHWRSFALLP--QEAPELVOLSHVLCGLLPLEI 139
Oy 132 --WVYFHLRLHNR--RIYKIHVHVEFOAFGEAYANPLETILGTGFFIGVILC 207
Db 140 FAKH-----LHUKVPLVYRPMKHONISSFALATQNPWELSLTFVDLJAVLR 194
Oy 208 DIRVILLANWTILLETIDVSGDIPLNPFLNLPF--YAGSRHDPHNFIGNYASTF 265
Db 195 CHPLTIFTHVNIWLSVEDHSGYDFPWSHRLVFPFGVGVVHNDHHSQFNCFAPYF 254
Oy 266 TMDRIPT 274
Db 255 TMDOKLGT 263

RESULT 9
US-09-177-419C-4
Sequence 2, Application US/09177419C
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: Russel, David W
APPLICANT: Lund, Erik G
TITLE OF INVENTION: Cholesterol 25-Hydroxylase
FILE REFERENCE: US/09177, 419C
CURRENT FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 4
LENGTH: 298
TYPE: PRT
ORGANISM: Mouse
US-09-177-419C-4

Query Match 17.6k; Score 290.5; DB 2; Length 298;
Best Local Similarity 28.5k; Pred. No. 3.3e-24;
Matches 71; Conservative 42; Mismatches 101; Indels 35; Gaps 8;
Oy 52 WGSIVHEAL-----YPLCLP-----GFLPQIPYMKYKIQNDPTEW 93
Db 24 WHLRSEALLOSFFVFIITTYGCLPVPVLDICSWVALRYKHDPSPSAO 83
Oy 94 OKCFVLLPHFICQPLICGTYTYTEYFNIPYMERHNPVYLLARCPCGCAVED 151
Db 84 LLPCGLGTYVHLVFPVTL--LHWRSFALLP--QEAPELVOLSHVLCGLLPLEI 139
Oy 132 --WVYFHLRLHNR--RIYKIHVHVEFOAFGEAYANPLETILGTGFFIGVILC 207
Db 140 FAKH-----LHUKVPLVYRPMKHONISSFALATQNPWELSLTFVDLJAVLR 194
Oy 208 DIRVILLANWTILLETIDVSGDIPLNPFLNLPF--YAGSRHDPHNFIGNYASTF 265
Db 195 CHPLTIFTHVNIWLSVEDHSGYDFPWSHRLVFPFGVGVVHNDHHSQFNCFAPYF 254
Oy 266 TMDRIPT 274
Db 255 TMDOKLGT 263

RESULT 8
US-09-177-419C-2
Sequence 2, Application US/09177419C
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: Russel, David W
APPLICANT: Lund, Erik G
TITLE OF INVENTION: Cholesterol 25-Hydroxylase
FILE REFERENCE: US/09177, 419C
CURRENT FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 272
TYPE: PRT
ORGANISM: human
US-09-177-419C-2

Query Match 17.1k; Score 281.5; DB 2; Length 272;
Best Local Similarity 28.5k; Pred. No. 3.3e-23;
Matches 72; Conservative 34; Mismatches 104; Indels 43; Gaps 7;
Oy 52 WGSIVHEAL-----YPLCLP-----GFLPQIPYMKYKIQNDPTEW 93
Db 24 WHLRSEALLOSFFVFIITTYGCLPVPVLDICSWVALRYKHDPSPSAO 83
Oy 94 OKCFVLLPHFICQPLICGTYTYTEYFNIPYMERHNPVYLLARCPCGCAVED 145
Db 84 LLPCGLGTYVHLVFPVTL--LHWRSFALLPHEAPPELLLLHLILFC 131
Oy 146 AVIEDTHYFHLRLHNR--RIYKIHVHVEFOAFGEAYANPLETILGTGFFIG 203
Db 132 LLPLD-HEFFVHLLHUKVPLRYTHKHONISSFALATQNPWELSLGFFDMHNV 190
Oy 204 VILCDHVLNANWTILLETIDVSGDIPLNPFLNLPF--YAGSRHDPHNFIGNY 261
Db 191 TLGCHPITLTHVNIWLSVEDHSGYDFPWSHRLVFPFGVGVVHNDHHSQFNCF 250
Oy 262 ASTFTMDRIPT 274
Db 251 APYTHMDRILOT 263

RESULT 9
US-09-949-016-7967
Sequence 7967, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: G. Craig et al.
TITLE OF INVENTION: POLYMERISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 7967

Query Match 17.1k; Score 281.5; DB 2; Length 275;
Best Local Similarity 28.5k; Pred. No. 3.3e-23;
Matches 72; Conservative 34; Mismatches 104; Indels 43; Gaps 7;
Oy 52 WGSIVHEAL-----YPLCLP-----GFLPQIPYMKYKIQNDPTEW 93
Db 27 WHLRSEALLOSFFVFIITTYGCLPVPVLDICSWVALRYKHDPSPSAO 86
Oy 94 OKCFVLLPHFICQPLICGTYTYTEYFNIPYMERHNPVYLLARCPCGCAVED 145
Db 87 LLPCGLGTYVHLVFPVTL--LHWRSFALLPHEAPPELLLLHLILFC 134
Oy 146 AVIEDTHYFHLRLHNR--RIYKIHVHVEFOAFGEAYANPLETILGTGFFIG 203
Db 135 LLPLD-HEFFVHLLHUKVPLRYTHKHONISSFALATQNPWELSLGFFDMHNV 193
Oy 204 VILCDHVLNANWTILLETIDVSGDIPLNPFLNLPF--YAGSRHDPHNFIGNY 261
Db 194 TLGCHPITLTHVNIWLSVEDHSGYDFPWSHRLVFPFGVGVVHNDHHSQFNCF 253
Oy 262 ASTFTMDRIPT 274
Db 254 APYTHMDRILOT 266

RESULT 10
US-09-439-554-22
Sequence 22, Application US/09439554
Patent No. 6479733
GENERAL INFORMATION:
APPLICANT: Rafalski, Jan Antoni
APPLICANT: Ocell, Joan T.
APPLICANT: Ocell, Joan T.
APPLICANT: Thorpe, Catherine J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
TITLE OF INVENTION: STEROL METABOLISM ENZYMES
FILE REFERENCE: B8114 US NA
CURRENT APPLICATION NUMBER: US/09/439,554
CURRENT FILING DATE: 1999-11-12

[illegible]

RESULT 15
 US 10/724,880-32
 Sequence 32, Application US/10724880D
 Patent No. 6869785
 GENERAL INFORMATION:
 APPLICANT: Ramodu, Omolayo O.
 APPLICANT: Orozco, Emil M.
 APPLICANT: Rafakati, J. Antoni
 APPLICANT: Shen, Jennie B.
 TITLE OF INVENTION: Sterol Metabolism Enzymes
 FILE REFERENCE: B81270205D
 CURRENT APPLICATION NUMBER: US/10/724,880D
 CURRENT FILING DATE: 2009-08-21
 PRIOR APPLICATION NUMBER: 09/743,041
 PRIOR FILING DATE: 2002-08-21
 PRIOR APPLICATION NUMBER: 60/109,293
 PRIOR FILING DATE: 1998-11-20
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn version 3.3

http://es.ScoreAccessWeb/GetItem.action?Appld=10753267&seqId=1105564&ItemName=20070205_152740_us-10-753-267-20.r... 2/8/07

[illegible]

Start _____ SC# 13 EMB#44 111772004

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

This page gives you Search Results detail for the Application 10753267 and Search Result 20070205_152734_us-10-753-267-20.rpr.

START

ScoreHomePage RefJelva Application List SCORE System Overview SCORE FAQ Comments / Suggestions

ON protein - protein search, using sw model
Run on: February 6, 2007, 05:42:54 ; Search time 42 Seconds
(without alignments)
671.226 Million cell updates/sec

Title: US-10-753-267-20
Perfect score: 1
Sequence: 1 MATSUSIFSSASIAVEV.....TDSQVAYNEKFEKTE 293
Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 01
Maximum Match 1001
Listing first 45 summaries

Database : PIR 80:
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:
Pred. No. is the number of results predicted by chance to have 4

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105563&ItemName=20070205_152734_us-10-753-267-20.r... 28/07

SCORE Search Results Details for Application 10753267 and Search Result 20070205_152734_us-10-753-267-20.rpr

38 91 5.5 336 2 721531 hypothetical prote
39 90.5 5.5 304 2 082189 conserved hypochet
40 90 5.5 732 2 002713 LIV-1 protein - hu
41 89.5 5.4 305 2 752111 atearoyl-CoA 9-des
42 89.5 5.4 307 2 A71605 probable integral
43 89 5.4 460 2 867134 hypothetical prote
44 88.5 5.4 322 2 A72066 hypothetical prote
45 88.5 5.4 751 2 T16355 major facilitator

ALIGNMENTS

RESULT 1
T18986 C-4 methyl sterol oxidase - fission yeast (Schizosaccharomyces pombe)
C1Species: Schizosaccharomyces pombe
C1Date: 03-Dec-1999 sequence_revision 03-Dec-1999 <text_change 09-Jul-2004
C1Accession: T18986
R1McDougal, R.C.; Rajandream, M.A.; Barrell, B.G.; Zimmermann, W.; Mambutti, R.
submitted to the EMBL Data Library, August 1999
A1Reference number: Z18122
A1Accession: T18986
A1Status: preliminary; translated from GB/EMBL/DBJ
A1Molecule type: DNA
A1Residues: 1-300 <END>
A1Cross-references: UNIPROT:Q9UUA; UNIPARC:UPI000012A0D5; EMBL:AL109832; P10N:CA52730.1; GSPDB:GM00066; SPDB:SPAC53
A1Experimental source: strain 972h-; cosmid c630
C1Genetics: T18986
A1Gene: SPDB:SPAC530.0BC
C1Superfamily: Saccharomyces cerevisiae ERG25 protein

Query Match 33.21; Score 548; DB 2; Length 300;
Best Local Similarity 36.71; Pred. No. 3.5e+43;
Matches 95; Conservative 60; Mismatches 72; Indels 32; Gaps 7;
Oy 54 SLIWHALYFLGCLGDFQFIPKMKYKIQKDFKQVFNKVFVLLVHPTQPLI 113
Db 52 SFLLHLLYFCGICPMHIDAMPYFRKRIQPKVPTLAQCECTVLLSHFTVLP 111
Oy 114 -----CCTTYTFEFTFYD-----VENFERNYFLARCFCACVIEDVHVFRLH 161
Db 112 WLFDPMCAFGTSLT-SVFPVPTNMQ-ITLFFEL-----EDNRYVHNLH 158

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105563&ItemName=20070205_152734_us-10-753-267-20.r... 28/07

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	548	33.2	300	2	T18986
2	536.5	32.5	309	2	probable C-4 methyl ERG25 protein - ye
3	517	31.4	253	2	probable C-4 sterol hypothetical prote
4	395.5	24.0	303	2	hypothetical prote
5	378	22.9	820	2	hypothetical prote
6	301	18.3	269	2	hypothetical prote
7	290	18.3	269	2	hypothetical prote
8	270.5	16.4	293	2	hypothetical prote
9	262	15.9	300	2	hypothetical prote
10	254	15.4	349	2	ERG25 protein - ye
11	234	14.2	258	2	probable sterol de
12	227.5	13.8	258	2	probable sterol de
13	204	12.4	274	2	C-5 sterol desatur
14	174	11.4	274	2	C-5 sterol desatur
15	167.5	10.2	231	2	hypothetical prote
16	164	9.9	329	2	probable desatur
17	162	9.8	344	2	C-5 sterol desatur
18	157	9.5	281	2	CER1-like protein
19	149	9.0	635	2	hypothetical prote
20	145	8.8	300	2	hypothetical prote
21	140.5	8.6	300	2	hypothetical prote
22	113.5	6.9	493	2	hypothetical prote
23	113	6.9	281	2	hypothetical prote
24	108.5	6.6	347	2	hypothetical prote
25	108	6.5	255	2	hypothetical prote
26	106	6.4	246	2	hypothetical prote
27	102.5	6.2	237	2	glossyl homolog -
28	101	6.1	555	2	glossyl protein gl
29	99	6.0	347	2	conserved hypochet
30	96	5.8	300	2	cytochrome o ubiqu
31	95.5	5.8	300	2	bo-type ubiquinol
32	94.5	5.7	663	2	bo-type ubiquinol
33	94.5	5.7	663	2	bo-type ubiquinol
34	94.5	5.6	455	2	cytochrome o ubiqu
35	92.5	5.6	455	2	cytochrome o ubiqu
36	92.5	5.6	455	2	cytochrome o ubiqu
37	91.5	5.5	300	2	hypothetical prote

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105563&ItemName=20070205_152734_us-10-753-267-20.r... 28/07

SCORE Search Results Details for Application 10753267 and Search Result 20070205_152734_us-10-753-267-20.rpr

Oy 162 HKRYKYIKYHNEFQPKQKAYNPRLTLLGCTGFTGICVALGD-----RVLLMAM 216
Db 159 YGTFYFTHVHRVSRAPGSAEYANPRLTLLGAGTVVPLKWCYFTHDILVTVYIW 218
Oy 217 VTIRLLETIDVSGDTDPLNPLMLIPFYAGSRHIDPHRKHFGYVASTFWFDRIFGDS 276
Db 219 ITLRLPQVDSIAGDTFWSLKLPLFMAGAHHDHTRHAKDNFSSFRWFDVATLDQ 278
Oy 277 QYNAVYNEK--EFKEKTE 291
Db 279 NYRQFKARLLAAKYAESK 297

RESULT 2
ERG25 C-4 methyl sterol oxidase - yeast (Saccharomyces cerevisiae)
W1Alternative names: protein G4158; protein YGR060W
C1Species: Saccharomyces cerevisiae
C1Date: 17-May-1996 <sequence_revision 17-May-1996 <text_change 09-Jul-2004
C1Accession: S64354
R1Enkian, K.D.; Rose, M.; Koettler, P.; Roehmer, A.; Seehsram, T.; Hempel, S.
submitted to the Protein Sequence Database, May 1996
A1Accession: S64354
A1Molecule type: DNA
A1Residues: 1-309 <END>
A1Cross-references: UNIPROT:P53045; UNIPARC:UPI000012A0D6; EMBL:Z72845; MID:g1323076; P10N:CAA97062.1; P10:g1323077;
A1Experimental source: strain 3288C
C1Genetics: ERG25
A1Gene: YGR060W
C1Superfamily: Saccharomyces cerevisiae ERG25 protein
C1Keywords: transmembrane protein
F1:51-67/Domain: transmembrane helix predicted <TM>
Query Match 32.51; Score 536.5; DB 2; Length 309;
Best Local Similarity 36.71; Pred. No. 3.5e+43;
Matches 112; Conservative 53; Mismatches 85; Indels 65; Gaps 8;
Oy 8 SIFSSASIA-----VEYUULLPENLQEPFKFKNYNNYNYTKYFOJATKGL- 55
Db 3 AFPHATLGLVQASTYQTLQVAPYQPOLPMKRYKAAVYSYNN-----DVLATLMP 58
Oy 56 -IVVEALYFLCLGDFQFIPKMKYKIQKDFKQVFNKVFVLLVHPTQPLI 114

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105563&ItemName=20070205_152734_us-10-753-267-20.r... 28/07

Db	59	TLHHEMYFNGCLPWITLDOIYFWRKLOPTKIPKAEQOLYCLKSLSHPLV-----112
Qy	115	GTYYTFYFNIPDNEKPNRYF-----LARGFCG-ADVETDHY 154
Db	113	-----SAPITWRINCEALGIVVEFFSLKTKALSIGLPLVLEDTNY 157
Qy	155	THLRLHKKRIYKYVHKVDFQAPQNGASVNPISLTLIGTGTFGIVGLCD-----208
Db	158	WNRILFMYGVFYKHKHRYAAPGLSAETASFAETLSLPGF-TVGNPLLYNMYGKL 216
Qy	209	WVLLNAAVYTLALLETLDVHGSGTQIDNPLNIPFYAGSRHHDPDHNFGIYATFTFW 268
Db	217	HLTLCVWITLALPQVDSIGSGTQFWSLKNIPFAGSAEHDLHHNYTIGNYASFRW 276
Qy	269	DRIQDTSQVNVYVHKKFEKTE 293
Db	277	DYLDQTSQPEAKASKEEMKKRAE 301

RESULT 3
 GR4695
 probable C-4 sterol methyl oxidase [imported] - Arabidopsis thaliana
 CSpecies: Arabidopsis thaliana (mouse-ear cress)
 CDate: 02-Feb-2001 sequence_revision 02-Feb-2001 text_change 09-Jul-2004
 AAccession: GR4695
 ATitle: cDNA clone, full-length
 AStem: 402 761-768 1999
 ATitle: Sequence number: A84420; M0083487; PMID:10617197
 AReference number: A84420; M0083487; PMID:10617197
 AAccession: GR4695
 AStatus: preliminary
 AStructure type: DNA
 AStructure: 1551 bp
 ACross-reference: UNIPROT:Q92422; UNIPARC:UFI000017A6C2; GR:AE002093; NID:g3980396; PIDN:AAC95159.1; GSPDB:GN00139
 CGenetics:
 A:Gene: At2g29390
 A:Map position: 2

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SCORE Search Results Details for Application 10753267 and Search Result 20070205 152734 us-10-753-267-20 rpr.

[illegible]

RESULT 5
 T04570
 hypochelical protein T12H17.140 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 sequence_revision 23-Apr-1999 text_change 09-Jul-2004
 C:Accession: T04570
 A:Accession: T12H17.140
 A:Author: T. H. Braun, M. Holzer, E. Brandt, A. Duesterhoeft, A. Bancroft, I. Nawas, H.M. Mayer, K.F. submitted to the Protein Sequence Database, February 1998
 A:Reference number: 215377
 A:Accession: T04570
 A:Molecule type: DNA
 A:Residues: 1-820 <REV>
 A:Experimental source: UNIPARC:UPI0000A6T06; EMBL:AL021635
 A:Experimental source: CULTIVAR Columbia; BAC clone T12H17

[illegible]

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[illegible]

RESULT 4
166618
hypothetical protein Pf6713.180 - *Arabidopsis thaliana*
C-Specific: *Arabidopsis thaliana* (mouse-ear cress)
C-Date: 23-Apr-1999 sequence_revision 23-Apr-1999 (stat_change 09-Jul-2004)
R-Accession: M14874
R-Accession: M14874
submitted to the Protein Sequence Database, April 1999
A-Reference number: 215789
A-Accession: T06618
A-Molecule type: DNA
A-Molecule type: cDNA
A-Accession: UNIPROT:Q98737; UNIPARC:UFI0000A0948; ENBL:AL049638; GSPD:
A-Experimental source: cultivar Columbia; BAC clone Pf6713

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A:1260
A:Map positions: 4
A:Introns: 112/3; 220/2; 265/3; 285/3
C:Superfamily: Saccharomyces cerevisiae ERG3 protein
Query Match: 24.0%; Score: 395.5; DB: 2;
Best Local Similarity: 32.0%; Prob. 0.48e-29;
Matches: 90; Conservative: 48; Mismatches: 104;
Matches: 90; Conservative: 48; Mismatches: 104;
43 NTFFQATGKLLVHVAALVPLGCFQTFY-----MKVYL 83
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SCORE Search Results Details for Application 10753267 and Search Result 20070205 152734 us-10-753-267-20.rpr.

QY	93	NQKRCRVLLFHHCFLQLPLCTGYTYTFYFNIPYME-----RNPRTVFL	138
DB	84	SNFKCTKDVN-----RNFLLVGPVLIQVYSPISQVDFPVFLQKMIISLIGLPLSCHEI	138
QY	139	LAMCGGCAVETWYTHVTHRLHHRHLYKYIKHSHQEPQFQMAHYAIPLETL	198
DB	139	VAQLVYFVSDYTNVHREKNCYKEXFTHIHREYTAPIGVAAFYAPVAVLLGIGIP	198
QY	199	FFGIGLVLCVHLWILWARYTLRLEETDVSGVDGFLFNLPLNLPFYAGSRHHDFHQHPT	258
DB	199	TEGLPAIFALPGLWALVLAQRIQALRETHSDFSTWFSMLTYPYIPYOGAAVHIDVH--WV	256
QY	259	G-----RPAATVTHFTHRIPTGDSQVAYNKKKVFYK	291
DB	257	GGGSGGSAFASVFTICDVIYTDGKGV-----RPPKK	286

RESULT 6
 T22413
 hypothetical protein F4912.9 - *Cannorhabdittis elegans*
 C-Species: *Cannorhabdittis elegans*
 C-Date: 15-Oct-1999 sequence_revision 15-Oct-1999 stext 09-Jul-2004
 C-Accession: T22413
 R-Thomas, K.
 submitted to the EMBL Data Library, October 1995
 A-Reference number: Z19565
 A-Accession: T22413
 A-Status: Preliminary; translated from GB/EMBL/DDBJ
 A-Residues: 1-269 [CUI>](#)
 A-Group-references: UNIPROT:Q20611; UNIPARC:UP1000007C133; EMBL: Z66520; PIDD: C
 A-Experimental source: clone F4912

[illegible]

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Db 23 GGTIVVHNPVRLNPLFTTIDMDPRQVQYKIOBKPKPLKYLKGLAVLANQF-1AG 81
Oy 111 PLIGGTYFTTFYF-----NIPYDWRNFWFLLARPCGAVI-EDWNYFLRLHHR 162
Db 82 PLITLFWFFAVFQFTGFLPGGQ-----IFRQIVISILCEBIFGYSHRLFHH 133
Oy 163 KRITKHKVHGFQAPQMEAYNAPLETLIG-TQFFIGVLGDVILWVILWAVTIRL 221
Db 134 PATVTHHRRHGRVAVTSITSCYCPLEALSNLSPLGLGTSNVTILXNASIA 193
Oy 222 LETIDVHSGVDPLPLNPLIPFYAGSRHDPHNNHFNIGYASTFTWDRIFQTDQYAY 281
Db 194 LATTCSHSGTH-----FPNLSPEPHYHKKVFWECFQGLLOW--HGTDSHF--- 240
Oy 282 HKKKKPKK 291
Db 241 ---RKSIEGK 247

RESULT 7

T12444
hypothetical protein F49E12.10 - *Cenozoobabditis elegans*
C:Species: *Cenozoobabditis elegans*
C:Accession: T12444
C:Date: 15-Oct-1999
C:Revision: 15-Oct-1999
C:Change: 09-Jul-2004
R:Thorne, K.
submitted to the EMBL Data Library, October 1995
A:Reference number: 219565
A:Accession: T12444
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Accession: U020612
A:Residues: 1-286 <WU>
A:Cross-references: UNIPROT:Q20612; UNIPARC:UP10000010B8D; EMBL:Z66520; PDB:CA91384.1; GSPDB:GN00070; CESP:F49E12.1
A:Experimental source: clone F49E12
C:Genetics:
A:Gene: CESP:F49E12.10
A:Map position: 2 130/2: 153/1: 221/3
C:Interact: T1272: 130/2: 153/1: 221/3
C:Superfamily: Saccharomyces cerevisiae ERG25 protein

Query Match 17.81; Score 293; DB 2; Length 286;
Best Local Similarity 29.81; Pred. No. 1.4e-19;
Matches 82; Conservative 40; Mismatches 109; Indels 44; Gaps 10;
Oy 29 LQSPKNNHNLNHTKYLATGSLI-VHEALFTLCLGLFLPQFI-----PNNKK 80

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SCORE Search Results Details for Application 10753267 and Search Result 20070205_152734_us-10-753-267-20.rpr

Db 8 LTTNPTVSVLSVPIVWASAFEFYHLPFVFKYHHPFEIARRHVPQAVK 67
Oy 100 VLKPHWC-----IQRLDGLG-----TYTTFYF--NIPYDWRP-----RWYF 137
Db 68 AVLPQCEVWVGLANPEYFEDANQKRYEAFSKNLPALLOVAFKPLATWF 127
Oy 138 LLA--LQCGAVTEQVYFURLHNR-KRITKHKVHGFQAPQMEAYNAPLETLI 194
Db 128 ITPAVQVTFATFIIDSGQVTHRTATKMLKLNHNNHNNLOVTFAGALNHPFGLI 187
Oy 195 LQSGFTGVLGCL-----DVLVLLWAVTIRLETDVHSGVDPLPLNPLIPYAGSRH 249
Db 188 LDT-PQAGVATLAAGLSPQAVIFF-----TLSTKTVDDHCYVFPYDPLQNF-FANNARY 242
Oy 250 HDPHNR--NFIGYAST-FTWDRIFQTF--DSQYNAHKKR-KFEKK 291
Db 243 NQDHPQVQVQNFQVFFTFWVGVGVGVNPPKSTPEKQKQANRR 291

RESULT 9

T16255
hypothetical protein F35C8.5 - *Cenozoobabditis elegans*
C:Species: *Cenozoobabditis elegans*
C:Accession: T16255
C:Date: 20-Sep-1999
C:Revision: 20-Sep-1999
C:Change: 09-Jul-2004
R:Wu, X.
submitted to the EMBL Data Library, November 1995
A:Reference number: 218486
A:Accession: T16255
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Accession: U020077
A:Residues: 1-300 <WU>
A:Cross-references: UNIPROT:Q20077; UNIPARC:UP1000007ED7C; EMBL:U40941; NID:q1072184; PID:q1072188; PDB:AAAB1710.1;
C:Genetics:
A:Gene: CESP:F35C8.5
A:Interact: 32/3: 62/1: 154/3: 184/3: 219/3
C:Superfamily: Saccharomyces cerevisiae ERG25 protein

Query Match 15.91; Score 262; DB 2; Length 300;
Best Local Similarity 15.91; Pred. No. 1.1e-16;
Matches 74; Conservative 44; Mismatches 97; Indels 76; Gaps 11;
Oy 27 NPLQEFFKNNMLNLTNFKTQIATGSLI-VHEALFTLCLGLFLPQFIIPNNKPK 85
Db 111 PLIGGTYFTTFYF-----NIPYDWRNFWFLLARPCGAVI-EDWNYFLRLHHR 162

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Db 2 LQELVTRVWFGDGVNLYVGVNAVAGISPLVLP-----PTIIDVDPKVP 53
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Db 54 YKIQKQRTWENQKCFKVLNHFICQLPLICGTYTTFYFNYIYDWR-----NPRW 107
Oy 136 YKIQKQRTWENQKCFKVLNHFICQLPLICGTYTTFYFNYIYDWR-----NPRW 195
Db 108 YKIQKQRTWENQKCFKVLNHFICQLPLICGTYTTFYFNYIYDWR-----NPRW 167
Oy 196 G-TQFFIGVLGDVILWVILWAVTIRLETDVHSGVDPLPLNPLIPYAGSRHDPH 254
Db 168 NUSFYAGVAFQVGVVSHYIPTSVAITTFPHSGM-----FPNLSPEPHYHKKVFW 219
Oy 255 NUSFYAGVAFQVGVVSHYIPTSVAITTFPHSGM-----FPNLSPEPHYHKKVFW 289
Db 220 KVF--NECVGFPLDMLHGTDTF-----RKSIE 246

RESULT 8

T40740
hypothetical integral membrane protein - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C:Accession: T40740
C:Date: 03-Dec-1999
C:Revision: 03-Dec-1999
C:Change: 09-Jul-2004
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lelaure, V.; Gallibert, P.
submitted to the EMBL Data Library, November 1998
A:Reference number: 221947
A:Accession: T40740
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Accession: U094598
A:Residues: 1-293 <LYN>
A:Cross-references: UNIPROT:Q94598; UNIPARC:UP1000006ACB1; EMBL:AL033388; PDB:CA21900.1; GSPDB:CH00067; SPDB:SPAC8
A:Experimental source: strain 972h-; cosmid c88
C:Genetics:
A:Gene: SPDB:SPAC87.15c
A:Map position: 2

Query Match 16.41; Score 270.5; DB 2; Length 293;
Best Local Similarity 30.11; Pred. No. 1.8e-17;
Matches 87; Conservative 41; Mismatches 110; Indels 51; Gaps 18;
Oy 49 IATWG---SLIVHEALFTL-CLPLGFLPQF-IPNNKRYKIQKQRTWEN---QKCFK 99
Db 111 PLIGGTYFTTFYF-----NIPYDWRNFWFLLARPCGAVI-EDWNYFLRLHHR 162

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105563&ItemName=20070205_152734_us-10-753-267-20.rpr 28/07

SCORE Search Results Details for Application 10753267 and Search Result 20070205_152734_us-10-753-267-20.rpr

Db 41 SPLPFPF-----VALSDITWVAVTTF-----IDVFLCH-VVFPKQAKIK 80
Oy 86 DHPETWENQKCFKVLNHFIC-----IQRLDGLG-----TYTTFYF--NIPYDWRP-----RWYF 137
Db 81 DRKVTMLKSKLQGNOLLVPMALVQLTWPTDPLPLAFTVPELHSLQALFFLA 140
Oy 123 PFIYDWRNFWFLLARPCGAVTEQVYFURLHNR-KRITKHKVHGFQAPQMEAYNAPLETLI 194
Db 141 PFTTFYF-----NIPYDWRNFWFLLARPCGAVI-EDWNYFLRLHHR 162
Oy 183 DAENVAPLETLIGTQFFIGV--LLCDHVVLLWAVTIRLETDVHSGVDPLPLNPLIPYAGSRH 249
Db 176 SAQHLRPFELFVGT--FTTTPWIFPHCLTYMFWFIAGSVYEVHICGTFPFAHRI 233
Oy 241 IPFYAGSRHDPHNNHFNIGYASTFTWDRIFQTF--DSQYNAHKKR-KFEKK 291
Db 234 PMYSGAPNDHNRHRLTFCQVFWYLYDLNG---VHTYADLKNTEAK 281

RESULT 10

S48533
SUR2 protein - yeast (*Saccharomyces cerevisiae*)
R:Alternate names: protein S48533; protein YDR297w; SUR2 protein
C:Species: *Saccharomyces cerevisiae*
C:Accession: S48533
C:Date: 02-Dec-1994
C:Revision: 02-Dec-1994
C:Change: 09-Jul-2004
R:Bonnen, M.
submitted to the EMBL Data Library, February 1994
A:Reference number: S48533
A:Accession: S48533
A:Status: Preliminary
A:Residues: 1-349 <RND>
A:Cross-references: UNIPROT:P38992; UNIPARC:UP10000136237; EMBL:U07171; NID:q458717; PID:q458718
C:Genetics:
A:Gene: SUR2
A:Interact: 32/3: 62/1: 154/3: 184/3: 219/3
C:Superfamily: Saccharomyces cerevisiae ERG25 protein
Query Match 15.91; Score 262; DB 2; Length 300;
Best Local Similarity 15.91; Pred. No. 1.1e-16;
Matches 74; Conservative 44; Mismatches 97; Indels 76; Gaps 11;
Oy 27 NPLQEFFKNNMLNLTNFKTQIATGSLI-VHEALFTLCLGLFLPQFIIPNNKPK 85
Db 111 PLIGGTYFTTFYF-----NIPYDWRNFWFLLARPCGAVI-EDWNYFLRLHHR 162

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105563&ItemName=20070205_152734_us-10-753-267-20.rpr 28/07

A:Accession: S48540
 A:Molecule type: DNA
 A:Residues: 1-3, 'K', 5-349 <CLI>
 A:Cross-references: UNIPARC:UP1000017B366; EMBL:U01427
 A:Comments: See also S48541
 A:Gene: SGD:SUR2; SVR2
 A:Cross-reference: SGD:S0002705; MIPS:YOR297w
 A:Map position: 4R
 A:Keywords: Transmembrane protein
 A:Cross-references: UniProtKB:Q99586; UniProtKB:Q99587
 F:95-115/Domain: transmembrane status predicted <TM>
 Query Match 15.4%; Score 254; Db 27; Length 349;
 Best Local Similarity 35.4%; Pred. No. 7.4e-16;
 Matches 37; Conservative 37; Mismatches 36; Indels 16; Gaps 8;

OY	141	KCFCAVIEDTNYFURLH-NKRIYKHVHHPQAFQFGEAEYHPLETLLTGTF	199
Db	160	KIFACPIYQVTFURLHNNKTLFYFVHLEWYPAQALNNPVEGLFDLT-L	218
OY	209	FTGIVLGLDGV-----TLAAWVYTLLETLTDHVSQDYLPLNPLIPFYAGSRHDFH	254
Db	219	GTGIAMTLTGHVLRHQEIIILFFAT--HRTVDHCICYPALDPEQVI-FPNNAVTHDIHR	274
OY	255	WVF--IGWVAF-FKQAFARICTDSDQVNAHKKKVEKKT	292
Db	275	QDGIKTNFAQPTFTNDNLDTN--FKGEVYKQKQKQKRV	313

[illegible]

http://es.ScoreAccessWeb/GetItem.action?Appld=10753267&seqId=105563&itemName=20070205_152734_us-10-753-267-20.r... 2/8/07

SSCORI: Search Results Details for Application 10753267 and Search Result 20070205 152734 us-10-753-267-20.rpt. Page 15 of 19

[illegible]

RESULT 13
EB7456
sterol desaturase family protein [imported] - Caulobacter crescentus
C-Species: Caulobacter crescentus
C-Accession: EB7456 sequence_revision 20-Apr-2001 feat_change 09-Jul-2004
R-Name: R-Nierman, M.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.; Alley, M.; Ohta, N.; Mead
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A-Title: Complete genome sequence of Caulobacter crescentus.
A-Reference: Nierman MC, Feldblum TV, Paulsen IT, Nelson KE, Eisen J, Heidelberg JF, Alley M, Ohta N, Mead D, et al. (2001) Proc Natl Acad Sci USA 98(16):4136-4141
A-Accession: AB749; NC_021173/69; F04B1125947
A-Status: preliminary
A-Molecule type: DNA
A-Molecule length: 1-174 cSTO
A-Cross-references: UNIPROT: Q9A799; UNIPARC: UPF00000CT478; GB: AE005673; NID: g1343079; PDB: ANK33449.1; GSPD: CH00148
A-Coarse-grained: SCG16?

```

Query Match      12.4%: Score 204: DB 2: Length 274:
Best Local Similarity 23.6%: Pred. No. 2.4e-11:
Matches 68: Conservative 35: Mismatches 107: Indels 78: Gaps 14:

OY      24 LPEPLDQ--PPKNN-----NMLNNTTKFQATGSLVHEALYPLCLGFLQFPIF 16
      111 66: 5: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
DB      1 NPKYKSLIPFANGLLIGWDIDYFAYFSIQW-----PVALVLLAKP----- 46
OY      27 NPKYKSL:GNKQKSTKQWKKQKFLVFNHFCIQ--PLICGTYTFYTFENIPLYDWMRMP 134

```

http://es.ScoreAccessWeb/CsItem.action?AppId=10753267&seqId=105563&itemName=20070205 152734 us-10-753-267-201... 2/8/07

[illegible]

RESULT 12
 B96716 sterol desaturase TC623.16 [imported] - Arabidopsis thaliana
 C1Species: Arabidopsis thaliana (mouse-ear cress)
 CDate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #stat_change 09-Jul-2004
 CAccession: B96716
 R1:Rethologia, A.; Ecker, J.R.; Palm, C.J.; Federzpie, N.A.; Kasl, S.; White, O.; Alonso, J.; Altier, H.; Araujo, R.; E
 Nature 408, 816-820, 2000
 A:Authors: Muner, J.; Jenkins, J.; Johnson-Hopson, C.; Wynn, S.; Klayton, S.; Kim, C.-J.; Koo, H.-L.; Kresnowatima,
 A:Authors: Schachtich, J.; R. Shino P.; Southwick, A.M.; Sam, R.; Tallon, L.J.; Tumbung, G.; Tortum,
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis -
 A:Reference number: A86141; NUID:20101619; PMID:11130712
 A:Accession: B96718
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-258 <370>
 C:Residues: UNIPROT:Q9PM42; UNIPARC:UFI0000048431; GI:AE005173; NID:q6665532; PIDN:AAF72931.1; GSPDB:GH00141
 C:Genes: TC623.16
 A:Map position: 1

http://es/ScoreAccessWeb/CellItem.action?AppId=10753267&seqId=1105563&itemName=20070205_152734_us-10-753-267-20.r...

SCORE Search Results Details for Application 10753267 and Search Result 20070205_152734_us-10-753-267-20.rpr.

Db 47 -MAGRIKHDTFRAGQ-----LLTEFASITSDVWVSTFGCLITGLFRAGKLP- 95

Qy 135 WYFLALRCFG-----CAVIEDTHVYFLRLHKKRIYKYIKVNHIEPQAPQMEA 184

Db 96 ---LAKGQWPFMSFLVLAITANDAMFTYTHMIDHSLRFTPHRHHSINPSPTA 152

Qy 185 EVAHRETLTLOETFGTGLGVGLVILM-----AMVTRILRLTIV-----HSCVD 232

Db 153 -YFLLGEALNALP-----VPLKLVLPFQPPVGLPLHGVIRNTLGHCEYE 200

Qy 233 IFLNPLM-----LIPTFAGSRHIDPHRHNFIGNYASTFTWDRIPQTD 275

Db 201 --LFFAKGDRFLPLTFTVTHDHLHQAQNGTGLYFTWDLKINGTE 246

RESULT 14

J01146

C-5 sterol desaturase (EC 1.-.-.-) - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: protein 12150; protein YLR056w

C:Species: *Saccharomyces cerevisiae*

C>Date: 31-Mar-1992 sequence revision 31-Mar-1992 #tax: 2004

C:Accession: J01146; 847993; 581630; 56488

C:Source: Genbank, L.G.: Shacter, P.L.: Guynn, C.J.: Barthuch, P.J.: Ulbright, C.E.: Bard, M. Gen 102 39-44, 1991

A:Title: Cloning, disruption and sequence of the gene encoding yeast C-5 sterol desaturase.

A:Residues: 1-365 <ART>
A:Crossa-references: UNIPARC:UF100001Z1A146; EMBL:N62623; NID:q171475
R:Renaldi, G., Lecrouette, F., Casarot, J.-P., Vandenheute, J., Delcour, J.
submitted to the EMBL Data Library, March 1992
A:Accession: 541593
A:Accession: 541593
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-365 <R>
A:Crossa-references: UNIPARC:UF100001Z1A146; EMBL:N64989; NID:q171476; PIDN:AA34595.1; PID:q171477
R:Uretsarazu, L.A.
submitted to the EMBL Data Library, December 1995
A:Accession: 561618
A:Accession: 561618
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-365 <UR>
A:Crossa-references: UNIPARC:UF100001Z1A146; EMBL:N94607; NID:q181264; PIDN:CA661303.1; PID:c21849; PID:q181277

http://es/ScoreAccessWeb/GetItem.action?AppId=10753267&seqId=1105563&ItemName=20070205_152734_us-10-753-267-20.r... 2/8/07

R.Andres, B.; Urzuzarazu, L.A.
submitted to the Protein Sequence Database, May 1996

A:Reference number: S64872
A:Accession: S64884
A:Molecule type: DNA
A:Accession: I-365-001
A:Codon table: standard
C:Note: experimental source strain S28BC
C:Comment: This enzyme introduces a C-5 double bond in the B ring of ergosterol.

C:Genetics:
A:Gene: SGD:ERG3; SYR1
A:Cosmid reference: SGD:S0004046; MIPS:YH056w
A:Feature: F12328
C:Keywords: oxidoreductase; transmembrane protein
F1234-109/Domain: transmembrane status predicted <TM>
F1294-270/Domain: transmembrane status predicted <TM>

Query Match 10.4% Score 171.5; DB 2; Length 365;
Query Match Similarity 23.4%; No. 3,5408;
Matches 63; Conservative 40; Mismatches 131; Indels 33; Gaps 7;

```
Oy   11 SSASLAVETGSLPQENLPQEFNNMUNTYTQTATGSGLVIR---EALYLEFLC 67
Db    : | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy   68 STFA-----SLPLSLLREFLEML-----VIVTIGLLTFTASTLSIFVF 120
Db    : | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy   76 PGTFPTPIPMNKYKIQDKETDEMGWCKFCIQLPCITGYFTFYETNFI 127
Db    : | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy   121 DEIPFNRPFLIKMMMEIKLASVAIW--HEMTVPVFMELNGSKLYMKRIDYEH-H 176
Db    : | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy   128 INEDNFNPYTLACGCAGVTEHTYTHLLHHRIKYKHVEHFQAFQGEAYIA 187
Db    : | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy   177 QVKILIIETVTITFDCCV-----YLNRGLINRVPAHKPHKKVLCTPFASHSF 230
Db    : | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy   188 HPLETLTGCTFGVICGLIVKMAWTTILLETIDVRSQDYDPLNHLPIIPFYGS 247
Db    : | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy   231 HPVGCGISIKHYPLIPAKHSYLLTPFTNYETIMHGQYSLNPPA-----VMGT 285
Db    : | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy   246 RHDFDPFRPGICWASTFWMDIEGT 274
Db    : | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy   286 ACHTVHLYENTNYQGDTLMWRDLGSS 312
Db    : | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Result 15
376372
hypothetical protein - Synchytrium sp. (strain PCC 6803)

http://es/ScoreAccessWeb/GetItem.action?AppId=10753267&seqId=105563&itemName=20070205_152734_us-10-753-267-20.r... 2/8/07

SCORE Search Results Details for Application 10753267 and Search Result 20070205 152734 us-10-753-267-20.rpr.

Page 19 of 19

start

<http://es.ScoreAccessWeb/GelItem.action?AppId=10753267&seid=105563&itemName=20170205%20152734%20us-10-753-267-20%20...>

20.5...

[illegible]

http://es/ScoreAccessWeb/CellItem.action?AppId=10753267&seqId=1105562&itemName=20070205_152729_us-10-753-267-20.r...

SCORE Search Results Details for Application 10753267 and Search Result 20070205 152729 us-10-753-267-20.rup.

CG	membrane; multi-pass membrane protein (Probable).	
CC	-1- DOMAIN: The histidine box domains may contain the active site	
CC	and/or be involved in metal ion binding (by similarity).	
CC	-1- SIMILARITY: Belongs to the sterol desaturase family.	
CC	Copyrighted by the Unifrost Consortium, see http://www.unifrost.org/Gene	
CC	http://www.unifrost.org/Gene	
CC	ENBL: CR660930; CAM51092.1; -: mRNA.	
DR	InterPro: IPR006097; Sterol_desatur.	
DR	InterPro: IPR006098; Sterol_desatur.	
DR	Flam: PF01598; Sterol_desat; 1.	
KW	Cellular reticulum; lipid synthesis; Membrane; NAD;	
KW	Oxidoreductase; Steroid biosynthesis; Sterol biosynthesis.	
KW	Transmembrane.	
FT	CHAIN 1 293 C-4 methylsterol oxidase.	
FT	Potential.	
FT	/FTIDEPRO_0000117035.	
FT	Potential.	
FT	Potential.	
FT	Histidine box-1 (By similarity).	
FT	MOTIF 157 161 Histidine box-2 (By similarity).	
FT	MOTIF 170 174 Histidine box-2 (By similarity).	
FT	MOTIF 249 255 Histidine box-3 (By similarity).	
FT	SEQUENCE 293 AA: 35216 MW: 38600 DBS55P96R CR664;	
QY	Query Match 100.0%; Score 1649; DB 1; Length 293;	
QY	Best Local similarity 100.0%; Pred. No. 1e-140;	
QY	Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

http://ee.ScoreAccessWeb/GetItem.action?AppId=10753767&seqId=1105562&ItemName=US-10-753-267-20 r 7/8/17

[illegible]

http://es/ScoreAccessWeb/GetItem.action?Appld=10753267&seqId=1105562&itemName=20070205_152729_us-10-753-267-20.r... 2/8/07

SCORE Search Results Details for Application 10753267 and Search Result 20070205 152729 us-10-753-267-20.rup.

```

241 1PTAYGSRBHNDPHNNFGVYASTTWDNRIGCTDSOYNVNKKKFKFKE 293
|||||
241 1PTAYGSRBHNDPHNNFGVYASTTWDNRIGCTDSOYNVNKKKFKFKE 293

RESULT SUMMARY
-----
AC      QM40A; MACFA PRELIMINARY: PHT: 293 AA.
TC
DT 17-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUN-2005, sequence version 1.
DE Brin CDNA, clone: GZRA-1285, similar to human sterol-C4-methyl
DE oxidase-like protein 1 (C4-beta oxidizing macaque) (Cynomolgus monkey).
DE OXPHOS; Nucleoside diphosphate kinase domain.
OC Eukaryota; Metazoa; Chordata; Cetartia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
NCBI_TaxID=9541;
RX
RN NC_016071DMS SEQUENCE.
EX
PE PubMed:15944441; DOI=10.1093/molbev/msh187.
PA Osaka M., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugeno S., Golobori T., Shen C.-K.J., Wu C.I., Hashimoto K.:
RA "Substitution Rate and Structural Divergence of 5'UTR Evolution:
RT Comparative Analysis Between Human and Cynomolgus Monkey cDNAs.";
RT Mol. Biol. Evol. 22:1976-1982(2005).
RG NC_016071DMS SEQUENCE.
RI International Consortium for macaque cDNA sequencing and analysis;
RP "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RT Submitted (JUN-2005) to the EMBL/GenBank/DBS databases.
CC Copyrighted by the UniProt Consortium. See http://www.uniprot.org/terms
CC and http://www.ncbi.nlm.nih.gov/policies/terms
CC -----
DR EMBL: AB169840; BA021921.1 -; mRNA.
DR GO: GO:00030424; Fcatalytic activity; IEA.
DR GO: GO:0008152; Fimbriabellum; IEA.
DR InterPro: IPR006087; Sterol_desat.
DR PROSITE: PS01569; Steroid desaturase.
DR SCOP: 1jz5; Steroid desaturase.
SD
SEQUENCE 293 AA. 3525 MW. 58ATGAGTGCTGCAGCG CRC64:

```

http://es/ScoreAccessWeb/GetItem.action?AppId=10753267&seqId=t105562&itemName=20070205 | 52729 us-10-753-267-20... 2/8/07

[illegible]

http://es/ScoreAccessWeb/GellItem.action?AppId=10753267&seqId=105562&itemName=20070205 152729 us-10-753-267-20.r... 2/8/07

30	SEQUENCE	291 AA:	34807 MW:	67A35386GF998116	CNC64:
	Query Match	82.3%	Score 1357:	Db 2:	Length 291:
	Beat Local Similarity	80.1%:	Pred. No. 2:	7e-114:	
	Matches 229:	Conservative 30:	Mismatches 27:	Indels 0:	Gaps 0:
Oy		1	MATHESVIFSSALANVYDLSLPKPTQEPFKANNVHLNPTQIATWGLSILVREA	60	
Oy		1	MEVWGNTALLSALVAVDSFSLPQRLQEPFKANNVHLNPTQIATWGLSILVREA	60	
Oy		61	LVYFLCLGFLGFTQPKMYKXIKDKETQENQWCKVFLPQPHRCIQLPLGCTGYT	120	
Oy		61	LVYFLCLGFLGFTQPKMYKXIKDKETQENQWCKVFLPQPHRCIQLPLGCTGYT	120	
Db		61	ITFLCFLGFTQFLPQPKMYKXIKDKETQENQWCKVFLPQPHRCIQLPLGCTGYT	120	
Oy		121	ETPHITQWENPRTVYLLAETGCAVIEDTHVYFLHLRHLKIKYTHKRVHESQAPF	180	
Db		121	ETPHITQWENPRTVYLLAETGCAVIEDTHVYFLHLRHLKIKYTHKRVHESQAPF	180	
Oy		181	GKEAYHAPLETLIGTGFTGVLGCLDHYLLAWAVYTLRLLETIDVHGSDYFLPFLKL	240	
Oy		181	GKEAYHAPLETLIGTGFTGVLGCLDHYLLAWAVYTLRLLETIDVHGSDYFLPFLKL	240	
Oy		241	QYAPCEBHDQDHWPTGVNSTATVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV	266	
Db		241	QYAPCEBHDQDHWPTGVNSTATVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV	266	
Db		241	IFETACGAPDHPHNPVGVSGSTFTTMDRLPDTGSGVNSVSHK	286	

RESULT 9
Q74H9.TETNG
ID Q74H9_TETNG PRELIMINARY; PRT: 276 AA.
AC Q74H9; integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DR 18-OCT-2005, GenBank.
DE Chromosome IX ICA9F981, whole genome shotgun sequence. [Fragment].
GN ORFNHase-GSTNHC00002130001.
OS Tetradonotus nigrovittidis (Green pufter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neoglyptari; Teleostei; Neoteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontinae; Tetraodon.
NCBI TaxID=99883.
PK NUCLEOTIDE SEQUENCE.
RP Published:15496914.DQI=10.1038/nature.03025;

...://ae/ScoreAgencyWeb/CustomAction?&url=115562&ItemName=300701205 152730 115-11-753-267-201 2/8/07

```

OC OC Eukaryote, Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OC AC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC CC Cyprinidae; Danio.
OC NC NCBI_TaxID=7955;
RW RW NUCLEOTIDE SEQUENCE.
CC CC TISSUE-whole body.
RX RX MEDLINE#223818257; PubMed=124779132; DOI=10.1073/pnas.242601899;
RX RA Strausberg R.L., Feilgenfeldt G.A., Grouse L.H., Derge J.S.,
RA KA Klausner H.D., Collins F.S., Wagner L., Shenmen C.M., Schuler C.D.,
RA Altshuler S.F., Zeng B.S., Bucio K.H., Scheffer C.R., Bat M.K.,
RA Chodura V.P., Brown W.B., Johnson R.E., McPherson P.R.,
RA Diatchenko L., Matsuda K.R., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshikuni S., Cantorci P., Prange C.,
RA Raja S.S., Lequellennec M.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Boak S.A., McGowan P.C., McKernan K.J., Malek J.A., Gunaratne P.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Marra M.A.,
RA Fahay J.J., Helton E., Kattman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
RA Blakeley R.V., Truchman J.W., Green D.E., Dickinson M.C.,
RA Rodriguez A.S., Gromicko J.J., Schmitt S., Myers R.M.,
RA Scherch A., Schrein J.E., Jones S.J.M., Merritt M.A.,
RT RT "Generation and initial analysis of more than 15,000 full-length human
RT RT and mouse cDNA sequences.";
RT RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RW RW [2] LEADORIDE SEQUENCE.
CC CC TISSUE-whole body.
CC CC Director: MCC Project.
RL RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC CC -----
CC CC Copyrighted by the UniProt Consortium. see http://www.uniprot.org/terms
CC CC and disclaimer. All rights reserved. No part may be reproduced without prior written
CC CC permission from The Creative Commons Attribution-NoDerivs License.
DR DR EMBL: BC050163; ANH50163.1; -; mRNA.
DR DR UniGene: Dr.12110; -.
DR DR ZFIN: ZDB-GENE-040426-2670; scfml.
DR DR GO: GO:0003824; Fcatalytic activity; IEA.
DR DR GO: GO:0003824; Fcatalytic activity; IEA.
DR DR InterPro: IPR006087; Steroid dehydratase domain.
DR DR InterPro: IPR006088; Sterol desatur.
DR DR RefSeq: PF01598; Sterol desatur. 1.

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[http://es.ScoreAccessWeb/GetItem.action?Appld=10753267&seqd=105562&itemName=20070205 152729 us-10-753-267-20.r...](http://es.ScoreAccessWeb/GetItem.action?Appld=10753267&seqd=105562&itemName=20070205%20152729%20us-10-753-267-20.r...) 2/8/07

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RA Maucell O., Aury J.-M., Brunet P. Petit J.-L., Stange-Thomann M.,
RA Nicoud B., Bouman R., Fischer C., Gout-Costa C., Bernot A.,
RA Nicaud B., Jaife D., Fisher S., Lurifolia G., Dossat C., Seguenhe B.,
RA Dasilva C., Salanoubat M., Levy M., Roudet M., Castellano B.,
RA Anthouard V., Jubin G., Castellani V., Katinka M., Vacherie B.,
RA Goumon C., Skall E., Bottonolou G., Bouhassira D., Berthod V.,
RA Goumon C., Skall E., Bottonolou G., Bouhassira D., Berthod V.,
RA Pariz G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Rosak S.,
RA Kellis M., Volff J.-M., Guigo R., Zody M.C., Meisior J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudez W., Schachter V., Quatier F., Saurin W., Scarpelli C.,
RA Linker S., Lander E.S., Weissenbach J., Rosset G., Collins M.,
RA The International Human Genome Sequencing Consortium.
RT The complete genome sequence of the human pathogen Leishmania
RT the early vertebrate photo-karyotype.
RL Nature 431:946-957(2004).
[2]
RP GENOSCOPE; Wellcome Institute Centre for Genome Research;
RP Genomes; Wellcome Institute Centre for Genome Research;
RP Genomes; Wellcome Institute Centre for Genome Research;
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBS whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC distributed under the terms of the UniProt License or the Open
CC Bioinformatics License, see http://www.uniprot.org/licenses.
CC
CC EMBL: CA601009581; CP92153.1; i: Genomic DNA.
CC GO: GO:0003824; F:catalytic activity; IEA.
CC GO: GO:0008152; P:metabolism; IEA.
CC DR DR: DR:IPR00087; S:sterol; deat.
CC DR DR: DR:IPR00088; S:sterol; deat.
CC DR DR: DR:IPR01598; S:sterol; deat. i
CC FT NON_TER
CC FT SEQUENCE 276 AA: 33397 MW: 08CB67A58916E75 CRC64:
CC
CC Query Match 79.3% Score 1308; DB 2: Length 276;
CC Query Match 79.3% Score 1308; DB 2: Length 276;
CC Query Match 79.3% Score 1308; DB 2: Length 276;
CC Matched 219; Conservative 28; Identical 0; Gaps
CC
QY 15 LAVEYDVSLLPFLNQLPQEFKFNANNVNTTFTGATGSLVIEALYFLCPGLFQF 74
DB 1 LAVEYDVAALPQLPQSLKAWGLNQLTFTTGTATGSLVIEALYFLCPGLFQF 60
QY 75 IYHVKYIKQKQNPETKQWQKVLNPHNCPDLPICCTGYTFTYFNIPDNEPR 134

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<http://es/ScoreAccessWeb/GetItem.action?AppId=10753267&seid=105562&itemName=20070205> | 52729 us-10-753-267-20.r...

db	1	MATHEVSIVIFSSALAVEVDSLLPENPLDPEFFKMANVYLLNNTYKQIATWGLVH6A	60
Oy	61	LYFLCLPGLPOTIPYKKYKIQNDPENWQKCFVLLNHFICQLPGLICGYTTF	120
db	61	LYFLCLPGLPOTIPYKKYKIQNDPENWQKCFVLLNHFICQLPGLICGYTTF	120
Oy	121	EYFNIPYDMEPRNRYVLLANGFCGAVIEDTWHYHRLHLHRRYKYYIKHVRHFEQAPF	180
db	121	EYFNIPYDMEPRNRYVLLANGFCGAVIEDTWHYHRLHLHRRYKYYIKHVRHFEQAPF	180
Oy	181	ORAEATAPLETLLIGTGGFFGIVLLCDVILLCORVILLWAMVTRILLETIDWHSQYDIPFLNLI	240
db	181	ORAEATAPLETLLIGTGGFFGIVLLCDVILLCORVILLWAMVTRILLETIDWHSQYDIPFLNLI	240
Oy	241	IPFYAGSRHNDPHNNFYIGNVASTFTWDRIPTGDSQVAYNKKRKKFEKTE	293
db	241	IPFYAGSRHNDPHNNFYIGNVASTFTWDRIPTGDSQVAYNKKRKKFEKTE	293
RESULT 2			
AD	AD56528	standard; protein: 293 AA.	
AC	AD56528		
DT	29-JAN-2004	(first entry)	
DE	Human Protein Q15800	SEQ ID NO 2382.	
XX	Human; pain; neuronal tissue; gene therapy;		
XX	spinal segmental nerve injury; chronic constriction injury; CCI;		
XX	spared nerve injury; SNI; Chung.		
OS	Homo sapiens.		
XX	W02003016475-A2.		
PD	27-FEB-2003.		
PF	14-AUG-2002	2002WO-05025765.	
XX	14-AUG-2001	2001US-0312147P.	
PR	01-NOV-2001	2001US-0346382P.	
XX	26-NOV-2001	2001US-0333347P.	

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105561&ItemName=20070205_152726_us-10-753-267-20.r... 2/8/07

Matches	293	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Oy	1	MATHEVSIFSSALAVEVDSLLPENPLDPEFFKMANVYLLNNTYKQIATWGLSVH6A	60						
Db	1	MATHEVSIFSSALAVEVDSLLPENPLDPEFFKMANVYLLNNTYKQIATWGLSVH6A	60						
Oy	61	LYFLCLPGLPOTIPYMKYKIQNDPENWQKCFVLLNHFICQLPGLICGYTTF	120						
Db	61	LYFLCLPGLPOTIPYMKYKIQNDPENWQKCFVLLNHFICQLPGLICGYTTF	120						
Oy	121	EYFNIPYDMEPRNRYVLLANGFCGAVIEDTWHYHRLHLHRRYKYYIKHVRHFEQAPF	180						
Db	121	EYFNIPYDMEPRNRYVLLANGFCGAVIEDTWHYHRLHLHRRYKYYIKHVRHFEQAPF	180						
Oy	181	ORAEATAPLETLLIGTGGFFGIVLLCDVILLCORVILLWAMVTRILLETIDWHSQYDIPFLNLI	240						
Db	181	ORAEATAPLETLLIGTGGFFGIVLLCDVILLCORVILLWAMVTRILLETIDWHSQYDIPFLNLI	240						
Oy	241	IPFYAGSRHNDPHNNFYIGNVASTFTWDRIPTGDSQVAYNKKRKKFEKTE	293						
Db	241	IPFYAGSRHNDPHNNFYIGNVASTFTWDRIPTGDSQVAYNKKRKKFEKTE	293						

RESULT 3			
AD	AD531647	standard; protein: 293 AA.	
AC	AD531647		
DT	29-JAN-2004	(first entry)	
DE	Human 6169 protein	450 ID 4.	
PR	Antitachycardic; caudant; vasotropic; antiinflammatory;		
PR	thrombolytic; antiarrhythmic; antitanginal; hypotensive; gene therapy;		
PR	cardiovascular; disorder; ischaemia; aortic bending;		
PR	vascular heart disease; endocarditis; aortic fibrillation; heart failure;		
XX	enlarged; cardiomyopathy; cardiac death.		
OS	Homo sapiens.		
XX	W02003065984-A2.		
PR	14-AUG-2003.		
XX	14-AUG-2003.		

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105561&ItemName=20070205_152726_us-10-753-267-20.r... 2/8/07

PA	(GENO) GEN HOSPITAL CORP.
XX	(FMR) BAYER AG.
PI	Woolf C, D'urao D, Befort K, Coatsign M;
XX	WPI: 2003-268312/26.
DR	GENBANK: Q15800.
XX	New composition comprising two or more isolated polypeptides, useful for
PT	preparing a medicament for treating pain in an animal.
XX	Claim 1: Page: 101pp: English.
PS	The invention discloses a composition comprising two or more isolated rat
CC	CC polypeptides or polypeptide derivatives which represent a fragment,
CC	CC derivative or allelic variation of the disclosed polypeptide. The
CC	CC claimed are a vector comprising the novel polynucleotide, a host cell
CC	CC comprising the vector, a method for identifying a nucleotide sequence
CC	CC which is differentially regulated in an animal subjected to pain and a
CC	CC kit to perform the method, an array, a method for identifying an agent
CC	CC that increases or decreases the expression of the polynucleotide sequence
CC	CC that is differentially expressed in neuronal tissue of a first animal
CC	CC and a method for identifying a polynucleotide sequence which is differentially
CC	CC expressed in an animal subjected to pain, a method for identifying a
CC	CC compound that regulates the activity of one or more of the
CC	CC polynucleotides, a method for producing a pharmaceutical composition, a
CC	CC method for identifying a compound or small molecule that regulates the
CC	CC activity in an animal of one or more of the polypeptides given in the
CC	CC present invention and/or identifying a compound useful in treating
CC	CC pain and a pharmaceutical composition comprising the compound and one or
CC	CC polypeptides or their antibodies. The polynucleotide or the compound that
CC	CC modulates its activity is useful for preparing a medicament for treating
CC	CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
CC	CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC	CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC	CC the specification) which is differentially expressed during pain. Note:
CC	CC This sequence is identical to the sequence presented in the prior art
CC	CC specification, but was obtained in electronic form directly from WIPO at
CC	CC ftp.wipo.int/pub/published_pct_sequences.
XX	cc ftp.wipo.int/pub/published_pct_sequences.
XX	Sequence 293 AA:
QY	Query Match 100.0% Score 1649; DB 7; Length 293;
DB	Best Local Similarity 100.0% Pseq. No. 3,4e-170;

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105561&ItemName=20070205_152726_us-10-753-267-20.r... 2/8/07

XX	29-JAN-2003	2003NO-US002571.
XX	01-FEB-2002	2002US-0353224P.
PR	15-MAR-2002	2002US-0364529P.
PR	19-APR-2002	2002US-0373861P.
PR	29-APR-2002	2002US-0376287P.
PR	12-JUN-2002	2002US-0386800P.
PR	14-JUN-2002	2002US-0386800P.
PR	03-JUL-2002	2002US-0394911P.
PR	10-JUL-2002	2002US-0394757P.
PR	21-AUG-2002	2002US-0404904P.
PR	23-AUG-2002	2002US-0405450P.
PR	06-NOV-2002	2002US-0424300P.
PR	05-DEC-2002	2002US-0431042P.
PR	05-DEC-2002	2002US-0431039P.
XX	(MILL-) MILLENNIUM PHARM INC.	
XX	Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghe M;	
PI	Stagliano N, Perodin J, Rodrigue-Way A;	
XX	WPI: 2003-731468/69.	
DB	H-PSDB: ADE31646.	
PT	Identifying a compound capable of treating a cardiovascular disorder	
PT	(e.g. atherosclerosis) comprises assaying the ability of the compound to	
PT	modulate the expression or activity of e.g. 1682, 6169 or 6193	
XX	polypeptide or nucleic acid.	
XX	Disclousre: SEQ ID NO 4; 328pp; English.	
CC	The invention relates to a method for identifying a compound capable of	
CC	CC treating a cardiovascular disorder. The present invention identifies the	
CC	CC differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,	
CC	CC 43226, 69292, 21656, 32427, 2402, 7747, 1720, 9351, 60491, 1371, 7077,	
CC	CC 345, 9253, 9135, 10537, 6530, 14745, 58446, 1870, 25836, 32394, 3484,	
CC	CC 2868, 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 51130,	
CC	CC 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or	
CC	CC 5985 genes in cardiovascular disease states. The methods are useful in	
CC	CC diagnosing, preventing and treating cardiovascular disorders, such as	
CC	CC atherosclerosis, cardiac hypertrophy, ischemia, reperfusion injury,	
CC	CC restenosis, arterial inflammation, vascular wall remodeling, coronary	

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105561&ItemName=20070205_152726_us-10-753-267-20.r... 2/8/07

QY 121 EYFNIPDYMERFVYLLARCGCAVEDTQWYFHLRLHKHRIKYIKYHVEFQAPF 180
DB 121 EYFNIPDYMERFVYLLARCGCAVEDTQWYFHLRLHKHRIKYIKYHVEFQAPF 180
QY 181 GHEAYNPLETLLIGTGFPGFVILGCHRVILLWMTYRLLETTIDVRSQYDIPLWJLH 240
DB 181 GHEAYNPLETLLIGTGFPGFVILGCHRVILLWMTYRLLETTIDVRSQYDIPLWJLH 240
QY 241 IFFTACSRHDFHNFNGYASTFTWDRIFGDSYWAYNEKKRKEKTE 293
DB 241 IFFTACSRHDFHNFNGYASTFTWDRIFGDSYWAYNEKKRKEKTE 293

RESULT 6
AD019683
ID AD019683 standard: protein; 293 AA.
AC AD019683;
XX 12-AUG-2004 (first entry)
DT 12-AUG-2004 (first entry)
DB Human PRO polypeptide #105.
XX Human; PRO; immune related disorder; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
XX systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
XX autoimmune hemolytic anemia; autoimmune thrombocytopenia; thyroiditis;
XX diabetes mellitus; renal disease; demyelinating disease;
XX demyelinating polyneuropathy; Guillain-Barre syndrome;
XX chronic inflammatory demyelinating polyneuropathy.
OS Homo sapiens.
XX WG2004043361-A2.
XX 27-MAY-2004.
XX 06-NOV-2003; 2003WO-US035268.
XX 06-NOV-2003; 2002US-0425235P.
XX (GETH) GENENTECH INC.
XX

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105561&ItemName=20070205_152726_us-10-753-267-20.rag 28/07

DB 181 GHEAYNPLETLLIGTGFPGFVILGCHRVILLWMTYRLLETTIDVRSQYDIPLWJLH 240
QY 241 IFFTACSRHDFHNFNGYASTFTWDRIFGDSYWAYNEKKRKEKTE 293
DB 241 IFFTACSRHDFHNFNGYASTFTWDRIFGDSYWAYNEKKRKEKTE 293

RESULT 7
AD088178
ID AD088178 standard: protein; 293 AA.
AC AD088178;
XX 21-OCT-2004 (first entry)
DT 21-OCT-2004 (first entry)
DB Human 6169 protein, an BR25 protein.
XX human; cardiovascular disorder; thrombotic disorder;
XX differential expression; gene therapy; aberrant vascularisation;
XX atherosclerosis; thrombosis; coronary artery disease; hyperlipidemia;
XX dyslipidemia; high blood pressure; heart failure; cardiast;
XX thrombolytic; anticoagulant; antilipemic; hypotensive; cardiant; BR25.
OS Homo sapiens.
XX WG2004063340-A2.
XX 29-JUL-2004.
XX 13-JAN-2004; 2004WO-US0000393.
XX 13-JAN-2003; 2003US-043683P.
XX 05-FEB-2003; 2003US-0445216P.
XX 18-FEB-2003; 2003US-0448036P.
XX 12-MAR-2003; 2003US-045189P.
XX 23-MAR-2003; 2003US-045341P.
XX 08-MAY-2003; 2003US-0469041P.
XX 10-JUN-2003; 2003US-0477414P.
XX 13-JUN-2003; 2003US-0478560P.
XX 24-JUL-2003; 2003US-0489772P.
XX 28-JUL-2003; 2003US-0490660P.
XX 03-SEP-2003; 2003US-0494938P.
XX 22-SEP-2003; 2003US-0504780P.

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105561&ItemName=20070205_152726_us-10-753-267-20.rag 28/07

PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
XX Wood W, Wu TD;
DR WPI: 2004-420067/39..
DR N-PSDB: AD019682.
XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO6388 useful for
PT treating immune related disorders such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthritis.
XX Claim 7: SEQ ID NO 610: 1731pp; English.
XX The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, autoimmune thrombocytopenia, autoimmune
CC hemolytic anemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC chronic inflammatory demyelinating polyneuropathy, Guillain-Barre
CC syndrome. This sequence represents a human PRO polypeptide of the
CC invention.
XX Sequence 293 AA:
QY 1 MATNESVIFSSASLAVEDVSLPENLQEPFKHANNVLLNHTYFQIATGSLIVHEA 60
DB 1 MATNESVIFSSASLAVEDVSLPENLQEPFKHANNVLLNHTYFQIATGSLIVHEA 60
QY 61 LYLFLCLPGTLPPTPKKKYKIQKRPETWEGKQCFKOLLPHNFCIQLPLIGCTYTF 120
DB 61 LYLFLCLPGTLPPTPKKKYKIQKRPETWEGKQCFKOLLPHNFCIQLPLIGCTYTF 120
QY 121 EYFNIPDYMERFVYLLARCGCAVEDTQWYFHLRLHKHRIKYIKYHVEFQAPF 180
DB 121 EYFNIPDYMERFVYLLARCGCAVEDTQWYFHLRLHKHRIKYIKYHVEFQAPF 180
QY 181 GHEAYNPLETLLIGTGFPGFVILGCHRVILLWMTYRLLETTIDVRSQYDIPLWJLH 240

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105561&ItemName=20070205_152726_us-10-753-267-20.rag 28/07

PI 24-SEP-2003; 2003US-0505510P.
PR 17-OCT-2003; 2003US-0512418P.
PR 27-OCT-2003; 2003US-0514660P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Scagliano NE, Healy A, Acton SL, Galvin KM, Donoghue MA;
XX Rogicway A, Tomlinson JE;
XX WPI: 2004-553729/53.
DR N-PSDB: AD088177.
XX Identifying a compound for treating a cardiovascular or thrombotic
PT disorder by combining a compound to be tested with e.g., a 9380, 9462,
PT 8701 or 2419 polypeptide or with a host cell expressing the polypeptide
PT and detecting the binding.
XX Claim 1: SEQ ID NO 20: 512pp; English.
XX This invention relates to a novel compound that is capable of treating a
CC cardiovascular or thrombotic disorder. Specifically, it refers to the
CC identification of nucleic acid molecules, and the encoded proteins
CC thereof, that are differentially expressed in cardiovascular disease
CC states. The invention describes test compounds (i.e. small molecules,
CC peptides or antibodies) that can bind to and modulate the activity of
CC these differentially expressed membrane-bound polypeptides, where binding
CC is detected by a competition binding assay, immunoassay or yeast two-
CC hybrid assay. Accordingly, pharmaceutical compositions can be developed
CC and used via gene therapy to treat aberrant vascularisation, hyperlipidemia,
CC dyslipidemia, high blood pressure or heart failure. As such, they
CC exhibit cardiant, thrombolytic, anticoagulant, antilipemic, hypotensive
CC and cardiant activities. This polypeptide sequence is a human protein
CC that is differentially expressed in a patient with a cardiovascular
CC disorder, given in an exemplification of the invention.
XX Sequence 293 AA:
QY 1 MATNESVIFSSASLAVEDVSLPENLQEPFKHANNVLLNHTYFQIATGSLIVHEA 60
DB 1 MATNESVIFSSASLAVEDVSLPENLQEPFKHANNVLLNHTYFQIATGSLIVHEA 60

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105561&ItemName=20070205_152726_us-10-753-267-20.rag 28/07

Db 1 MATNESVIFSSASLAVYVDSLLPENLQEPFRKNNYNNLNTYKQIATGSLIVHEA 60
Oy 61 LVFLPCPLGFLPQIPYMKYKIQKDEPTEWQKCFVLLPNHFCIQPLICGTYYTF 120
Db 61 LVFLPCPLGFLPQIPYMKYKIQKDEPTEWQKCFVLLPNHFCIQPLICGTYYTF 120
Oy 121 EYFMFYDMERNPNTYLLANCPGCAVIEDTHYFLRLHLHKRIYKIKYKHYREFOQPF 180
Db 121 EYFMFYDMERNPNTYLLANCPGCAVIEDTHYFLRLHLHKRIYKIKYKHYREFOQPF 180
Oy 181 GMEAYANPLETLLIGTGFPGVLLCDRVLLMAWVTIRLLETIDVHSGVDIPLPNHL 240
Db 181 GMEAYANPLETLLIGTGFPGVLLCDRVLLMAWVTIRLLETIDVHSGVDIPLPNHL 240
Oy 241 IFFPAGSRHDFHNNFTIGNYASTFTTWMDRIPTGDSQYVANKKKFEKTE 293
Db 241 IFFPAGSRHDFHNNFTIGNYASTFTTWMDRIPTGDSQYVANKKKFEKTE 293

RESULT 8
ID ADP56122 standard: protein: 293 AA.
AC ADP56122;
DT 18-NOV-2004 (first entry)
DE Human PRO protein sequence 950 ID NO:2098.
XX human: PRO; immune related disease; inflammatory immune response;
XX congenital hemidysplasia; ichthyosiform erythroderma and limb defects;
XX antithrombotic; antidiabetic; antineoplastic; antiparasitic; antiproliferative;
XX antithrombotic; antidiabetic; antineoplastic; antiparasitic; antiproliferative;
XX haemostatic; hepatotropic; CNS; dermatological; gastrointestinal;
XX nephrotropic; neuroprotective; osteoporotic; immunosuppressive; muscular;
XX virulent; gene therapy.
XX Homo sapiens.
XX W0200403956-A2.
XX 13-MAY-2004.
PF 28-OCT-2003: 2003MO-U5034381.
XX

50 Sequence 293 AA:
Query Match 100.0%; Score 1649; DB 8; Length 293;
Best Local Similarity 100.0%; Pred. No. 3-4e-170;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MATNESVIFSSASLAVYVDSLLPENLQEPFRKNNYNNLNTYKQIATGSLIVHEA 60
Db 1 MATNESVIFSSASLAVYVDSLLPENLQEPFRKNNYNNLNTYKQIATGSLIVHEA 60
Oy 61 LVFLPCPLGFLPQIPYMKYKIQKDEPTEWQKCFVLLPNHFCIQPLICGTYYTF 120
Db 61 LVFLPCPLGFLPQIPYMKYKIQKDEPTEWQKCFVLLPNHFCIQPLICGTYYTF 120
Oy 121 EYFMFYDMERNPNTYLLANCPGCAVIEDTHYFLRLHLHKRIYKIKYKHYREFOQPF 180
Db 121 EYFMFYDMERNPNTYLLANCPGCAVIEDTHYFLRLHLHKRIYKIKYKHYREFOQPF 180
Oy 181 GMEAYANPLETLLIGTGFPGVLLCDRVLLMAWVTIRLLETIDVHSGVDIPLPNHL 240
Db 181 GMEAYANPLETLLIGTGFPGVLLCDRVLLMAWVTIRLLETIDVHSGVDIPLPNHL 240
Oy 241 IFFPAGSRHDFHNNFTIGNYASTFTTWMDRIPTGDSQYVANKKKFEKTE 293
Db 241 IFFPAGSRHDFHNNFTIGNYASTFTTWMDRIPTGDSQYVANKKKFEKTE 293

RESULT 9
ID ADR68904 standard: protein: 293 AA.
AC ADR68904;
DT 18-NOV-2004 (first entry)
DE Human C-4 sterol methyloxidase protein.
XX beta-hydroxysteroid dehydrogenase; beta-HSD; NSDHL;
XX CHILD syndrome; skin disorder; psoriasis; ichthyosis; bone defects;
XX osteoporosis; osteocleorosis; eye disorder; cataract; macrophthalmia;
XX arthritis; human: C-4 sterol methyloxidase; enzyme.
XX Homo sapiens.
XX

PF 28-OCT-2003: 2003JUS-0421472P.
XX (GETH) GEMENTECH INC.
PA Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
PI Wood WJ, Wu TD;
XX WPT: 2004-37402/35.
DB N-PSDB; ADP56121.
XX
XX New PRO polynucleotides and polypeptides, useful in diagnosing
XX and treating an immune related disease, e.g. systemic lupus
XX erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
XX stimulating an immune response.
XX Claim 1: SEQ ID NO 2098, 3009pp; English.
XX
XX The present invention describes an isolated PRO nucleic acid (1). Also
XX described: (1) a vector comprising (1); (2) a host cell comprising the
XX vector of (1); (3) a process for producing a PRO polypeptide; (4) an
XX isolated PRO polypeptide; (5) a chimeric molecule comprising the
XX polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
XX antibody or antigenically binding molecule to a polypeptide of (4); (7) a
XX composition of at least one of the polypeptides of (4) and (6) or
XX antagonist of the polypeptide or an antibody that binds to the
XX polypeptide in combination with a carrier; (8) an article of manufacture
XX comprising a container, a label on the container and a composition of
XX matter of (7); (9) a method of treating an immune related disease in a
XX mammal; (10) a method for determining the presence of a PRO polypeptide
XX in a sample suspected of having the polypeptide; (11) a method of
XX using the polypeptide or antibody for diagnosing an immune response
XX in a mammal; (12) a method of identifying a compound that inhibits or
XX mimics the activity of or expression of a gene encoding a PRO polypeptide
XX; and (13) a method of stimulating the immune response in a mammal. The
XX PRO sequences have antitumor, antineoplastic, antiparasitic,
XX antithrombotic, antidiabetic, CNS, dermatological, gastrointestinal,
XX haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
XX nephrotropic, neuroprotective, osteoporotic, immunosuppressive, and
XX virulent activities, and can be used in gene therapy. The nucleic acid
XX (1) and the encoded polypeptides, compositions, kits and methods are
XX useful in diagnosing and treating an immune related disease and in
XX stimulating an immune response. The present sequence represents a human
XX PRO protein from the present invention.
XX

XX U52004166465-A1.
XX
XX 26-AUG-2004.
PF 14-OCT-2003: 2003JUS-00664978.
XX
XX 01-JUN-1999: 9905-0137020P.
PR 01-JUN-2000: 200005-00584976.
PR 03-SEP-2001: 2003JUS-0094606.
XX (CHIL-) CHILDRENS HOSPITAL INC.
XX
XX Herman GE, Kelley RI, Grange DK;
XX
XX WPI: 2004-034389/61.
DB N-PSDB; ADR68903.
XX
XX Diagnosing congenital hemidysplasia, ichthyosiform erythroderma and limb
XX defects syndrome in patient, by isolating patient's NSDHL polynucleotide,
XX detecting nucleotide difference between patient's NSDHL and wild-type
XX NSDHL gene.
XX
XX Disclosure: SEQ ID NO 6; 23pp; English.
XX
XX The present invention relates to beta-hydroxysteroid dehydrogenase
XX (beta-HSD; NSDHL) involved in the conversion of 4,4-dimethylcholesterol-8(9)
XX -en-3beta-ol to cholesterol in the cholesterol and vitamin D
XX biosynthetic pathway. The invention is useful in the diagnosis of
XX congenital hemidysplasia, ichthyosiform erythroderma and limb defects
XX (CHILD) syndrome, skin disorders such as psoriasis and ichthyosis, bone
XX defects and osteoporosis, osteocleorosis, eye disorder, cataract, macrophthalmia,
XX arthritis and microphthalmia, arthritis and diagnosing disease states that
XX are associated with mutations in the NSDHL gene encoding proteins that
XX are involved in the cholesterol and/or vitamin D biosynthetic pathway.
XX The present sequence is the human C-4 sterol methyloxidase protein.
XX
XX Sequence 293 AA:

Query Match 100.0%; Score 1649; DB 8; Length 293;
Best Local Similarity 100.0%; Pred. No. 3-4e-170;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MATNESVIFSSASLAVYVDSLLPENLQEPFRKNNYNNLNTYKQIATGSLIVHEA 60
Db 1 MATNESVIFSSASLAVYVDSLLPENLQEPFRKNNYNNLNTYKQIATGSLIVHEA 60

OY 61 LVFLCFLGFLQFIPYMKYKIQDKPEWQKQKFKVLLPNFCIQPLICGTYTFF 120
DB 61 LVFLCFLGFLQFIPYMKYKIQDKPEWQKQKFKVLLPNFCIQPLICGTYTFF 120
OY 121 EYFNIPTWEMPRNYELARCGCAVIEDWRYFJRLHLHKRIYKYIKYHVEFQAPF 180
DB 121 EYFNIPTWEMPRNYELARCGCAVIEDWRYFJRLHLHKRIYKYIKYHVEFQAPF 180
OY 181 GMEAEYANPLETLLGTFGFIQVLLCDRYVLLWAVYTRILETIDVHSGYDIFLPLJL 240
DB 181 GMEAEYANPLETLLGTFGFIQVLLCDRYVLLWAVYTRILETIDVHSGYDIFLPLJL 240
OY 241 IFTFAGSHHDPHNNFIGNYASTFTWDRIFGDSQYVAYNKKRKKFEKTE 293
DB 241 IFTFAGSHHDPHNNFIGNYASTFTWDRIFGDSQYVAYNKKRKKFEKTE 293
RESULT 10
ID ADP24211 standard: protein: 293 AA.
XX PRO: antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
XX oncoprotein; antidiabetic; antidiabetic; antidiabetic; antidiabetic;
XX antineutrophic; hepatotropic; respiratory; gene therapy; immune system.
O3 Unidentified.
XX W02000041170-A2.
XX 21-MAY-2004.
XX 30-OCT-2003; 2003NO-US034312.
XX 01-NOV-2002; 2002US-0423394F.
XX (GETH) GEMTECH INC.
P1 Clark N. Schoenfeld J. Van Lookeren M. Williams PM. Wood WJ.

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105561&ItemName=20070205_152726_us-10-753-267-20.r... 28/07

OY 1 MATHESV1IFSSASLAVEYDILLPENLQEPFKNANNPLNNYTKFOJATWGLIVHEA 60
DB 1 MATHESV1IFSSASLAVEYDILLPENLQEPFKNANNPLNNYTKFOJATWGLIVHEA 60
OY 61 LVFLCFLGFLQFIPYMKYKIQDKPEWQKQKFKVLLPNFCIQPLICGTYTFF 120
DB 61 LVFLCFLGFLQFIPYMKYKIQDKPEWQKQKFKVLLPNFCIQPLICGTYTFF 120
OY 121 EYFNIPTWEMPRNYELARCGCAVIEDWRYFJRLHLHKRIYKYIKYHVEFQAPF 180
DB 121 EYFNIPTWEMPRNYELARCGCAVIEDWRYFJRLHLHKRIYKYIKYHVEFQAPF 180
OY 181 GMEAEYANPLETLLGTFGFIQVLLCDRYVLLWAVYTRILETIDVHSGYDIFLPLJL 240
DB 181 GMEAEYANPLETLLGTFGFIQVLLCDRYVLLWAVYTRILETIDVHSGYDIFLPLJL 240
OY 241 IFTFAGSHHDPHNNFIGNYASTFTWDRIFGDSQYVAYNKKRKKFEKTE 293
DB 241 IFTFAGSHHDPHNNFIGNYASTFTWDRIFGDSQYVAYNKKRKKFEKTE 293

CELL INK1 2004

SCORE 1.2 Build Date: 12/12/2006

P1 No TD:
XX WFI: 2004-415628/39.
DR N-PSDB: ADP24210.
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX Claim 7: SEQ ID NO 1389: 294Opp: English.
XX The invention relates to a novel isolated nucleic acid and the PRO
polypeptide encoded by it. A protein of the invention has
CC antineutrophic, antidiabetic, antirheumatic, immunosuppressive,
CC oncoprotein, antidiabetic, antidiabetic, antidiabetic, antidiabetic;
CC antineutrophic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC idiopathic chronic arthritis, spondyloarthritis, systemic sclerosis, an
CC inflammatory bowel disease, autoimmune hemolytic anemia, autoimmune
CC vasculitis, sarcoidosis, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC inflammatory bowel disease, glutamate-related neurological disorder,
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis; food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, heart transplantation associated disease, graft rejection or
CC rejection of a heart, a heart disease. The present sequence represents a PRO protein
CC of the invention.
XX Sequence 293 AA:
Query Match 100.0%; Score 1649; DB 8; Length 293;
Best Local Similarity 100.0%; Pred. No. 3,4e-170; Indels 0; Gaps 0;
Matches 293; Conservative 0; Mismatches 0;

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1105561&ItemName=20070205_152726_us-10-753-267-20.r... 28/07


```
Db 1261 ATCTAGGCTTTCTCCGATTAAGCATAGGCTGGAAGTTCAGCATTTGGGCTTTAAATC 1320
Oy 1321 TTTAGATATAGTGGTATTTTCAGAAATTTCTCATAGTGGTATGGGCTATATATTA 1380
Db 1321 TTTAGATATAGTGGTATTTTCAGAAATTTCTCATAGTGGTATGGGCTATATATTA 1380
Oy 1381 ACTGTTTATATTTTATTTTTCAGACAGGACCAACATCTCTCTGCTGGCTGGAGTC 1440
Db 1381 ACTGTTTATATTTTATTTTTCAGACAGGACCAACATCTCTCTGCTGGAGTC 1438
Oy 1441 TGTGGCAGAGTCTCACTCACTC 1465
Db 1439 TGTGGCAGAGTCTCACTCACTC 1463

RESULT 3
US-10-533-519-1388
: Sequence 1388, Application US/10533519
: Publication No. US2006026377A1
: GENERAL INFORMATION:
: APPLICANT: CLARK, RILEY
: INVENTOR: CLARK, RILEY
: APPLICANT: VANJOEREN, MENDO
: APPLICANT: WILLIAMS, P. MICKEY
: APPLICANT: WOOD, WILLIAM J.
: APPLICANT: WU, THOMAS D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS OF THE TREATMENT OF INJURY
: TITLE OF INVENTION: RELATED DISEASES
: CITE REFERENCES: P194H1 US
: CURRENT FILING DATE: 2005-04-28 US/10/533-519
: PRIOR FILING DATE: 2005-04-28
: PRIOR APPLICATION NUMBER: PCT/US03/34312
: PRIOR FILING DATE: 2003-10-30
: PRIOR APPLICATION NUMBER: US 60/423,394
: PRIOR FILING DATE: 2002-11-01
: NUMBER OF SEQ ID NOS: 2517
: SEQ ID NO 1: 1388
: LENGTH: 1384
: TYPE: DNA
: ORGANISM: Homo sapien
US-10-533-519-1388

Query Match 94.4%; Score 1383.4; DB 6; Length 1384;
Best Local Similarity 99.6%; Pred. No. 6, le-252;
```

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089420&ItemName=20070202_145122_us-10-753-267-19.t... 28/07

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Oy 727 GTTGGGATGGGATGATGATGATTTAGAAATATGATGATGATGATGATGATGAT 786
Db 661 GTTGGGATGGGATGATGATGATTTAGAAATATGATGATGATGATGATGATGAT 720
Oy 787 ATTCCTCTACAGCTTTAAATCGATGCTTCTATGCTGGTTCGGCATCATGATTC 846
Db 721 ATTCCTCTACAGCTTTAAATCGATGCTTCTATGCTGGTTCGGCATCATGATTC 780
Oy 847 CACCATATGATCTTGGAAAGATGCTTCACATTTTACATGCTGGATCGAATTTT 906
Db 781 CACCATATGATCTTGGAAAGATGCTTCACATTTTACATGCTGGATCGAATTTT 840
Oy 907 GGAAGAGCTCTCATATATGCTCATATGAAAGAGGAGAGTTCGAGAAAAGACT 966
Db 841 GGAAGAGCTCTCATATATGCTCATATGAAAGAGGAGAGTTCGAGAAAAGACT 900
Oy 967 GAATATATCTCATATATGCTCATATGAAAGAGGAGAGTTCGAGAAAAGACT 1026
Db 901 GAATATATCTCATATATGCTCATATGAAAGAGGAGAGTTCGAGAAAAGACT 960
Oy 1027 GTAGTACATATCTCTTGGAGAGGAATAGCATGCTCTGCTGCTACTAGTGATTA 1086
Db 961 GTAGTACATATCTCTTGGAGAGGAATAGCATGCTCTGCTGCTACTAGTGATTA 1020
Oy 1087 AAGAGCAATTAAGCAATTTAATTAAGTCTCTGCTGGAGACTTTTCTACTTACTACA 1146
Db 1021 AAGAGCAATTAAGCAATTTAATTAAGTCTCTGCTGGAGACTTTTCTACTTACTACA 1080
Oy 1147 AGTCTCATATATGATGAATGAATTAATATATTAAGTACAGATTTTCATAGGAGTT 1206
Db 1081 AGTCTCATATATGATGAATGAATTAATATTAAGTACAGATTTTCATAGGAGTT 1140
Oy 1207 TTAAGAGCATGCTTCTAGTCTGAGAGGAATTTGGATCTAGAGATTAATCTAT 1266
Db 1141 TTAAGAGCATGCTTCTAGTCTGAGAGGAATTTGGATCTAGAGATTAATCTAT 1200
Oy 1267 GCGTTTCTGCGATTAAGCATATAGGCTGAAGTCAATATGGGCTTTAAATCTTTAG 1326
Db 1201 GCGTTTCTGCGATTAAGCATATAGGCTGAAGTCAATATGGGCTTTAAATCTTTAG 1260
Oy 1327 ATATATAGTGGCATTTTCAGAAATTTCTCATAGTGGTATGGGCTATATTAATCTTT 1386
Db 1261 ATATATAGTGGCATTTTCAGAAATTTCTCATAGTGGTATGGGCTATATTAATCTTT 1320
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http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089420&ItemName=20070202_145122_us-10-753-267-19.t... 28/07

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Matches 1396; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
Oy 67 AGGCTGCTGCAGAGATTTGAANAATGGCAAAATGATGTCAGCATCTTTAGTTCA 126
Db 1 AGGCTGCTGCAGAGATTTGAANAATGGCAAAATGATGTCAGCATCTTTAGTTCA 60
Oy 127 GCATCTCTGGCTGGATATGTAGATTCATTTTACCTGAGAGATCTCTCGAGAGCA 186
Db 61 GCATCTCTGGCTGGATATGTAGATTCATTTTACCTGAGAGATCTCTCGAGAGCA 120
Oy 187 TTTAANAATGGCTGGACATATGTGATTAATTAATACAAAGTTCAGATTCGACATG 246
Db 121 TTTAANAATGGCTGGACATATGTGATTAATTAATACAAAGTTCAGATTCGACATG 180
Oy 247 GGATCGCTTATAGTATGAAAGCTTTATTTCTATCTGTTACTGGATTTTATTT 306
Db 181 GGATCGCTTATAGTATGAAAGCTTTATTTCTATCTGTTACTGGATTTTATTT 240
Oy 307 CAATTTATAGCTATATGAANAATACAAAMATTCAAGATATAGCAGAGATGGCA 366
Db 241 CAATTTATAGCTATATGAANAATACAAAMATTCAAGATATAGCAGAGATGGCA 300
Oy 367 AACATAGGAAGTCTTCAAAAGTCTCTCTTAATCACTCTGATTCGAGCTGCTTTC 426
Db 301 AACATAGGAAGTCTTCAAAAGTCTCTCTTAATCACTCTGATTCGAGCTGCTTTC 360
Oy 427 ATTTGCGAACCTATATTTACAGAGATTTTCATATATCTTATGATTCGAGAGATG 486
Db 361 ATTTGCGAACCTATATTTACAGAGATTTTCATATATCTTATGATTCGAGAGATG 420
Oy 487 CCAAGATGGATTTCTTTGCGAAGATGCTTGGTGGAGTATGAGATACCTGCTG 546
Db 421 CCAAGATGGATTTCTTTGCGAAGATGCTTGGTGGAGTATGAGATACCTGCTG 480
Oy 547 CACTATTTCTGCTAGATCTTACACCAAAAGATATACAGATATATTCATAAGTT 606
Db 481 CACTATTTCTGCTAGATCTTACACCAAAAGATATACAGATATATTCATAAGTT 540
Oy 607 CATCATGATCTAGGCTGCAATTTGGATGCGAATGATGATGCAATCTCTTGGAGACT 666
Db 541 CATCATGATCTAGGCTGCAATTTGGATGCGAATGATGATGCAATCTCTTGGAGACT 600
Oy 667 CTAAATCTGGAATGATTTTTCATGGAATGCTGCTTTGTGTGATCATGATATCTT 726
Db 601 CTAAATCTGGAATGATTTTTCATGGAATGCTGCTTTGTGTGATCATGATATCTT 660
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http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089420&ItemName=20070202_145122_us-10-753-267-19.t... 28/07

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Oy 1387 TTTTATTTTTTTTGGAGCAAGGCAAGCACTCTCTCTGGCTGGAGTGGTGG 1446
Db 1321 TTTTATTTTTTTTGGAGCAAGGCAAGCACTCTCTCTGGCTGGAGTGGTGG 1378
Oy 1447 CACAGTCTCAGCTCACTGCTC 1465
Db 1379 CACAGTCTCAGCTCACTGCTC 1397

RESULT 4
US-10-537-121-10
: Sequence 10, Application US/10537121
: Publication No. US2006026937A1
: GENERAL INFORMATION:
: APPLICANT: diadexus, Inc.
: INVENTOR: Turner, Leah
: APPLICANT: Turner, Leah
: APPLICANT: Turner, Leah
: TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Proteins
: FILE REFERENCE: DEX-0449
: CURRENT APPLICATION NUMBER: US/10/537,121
: PRIOR FILING DATE: 2005-06-02
: PRIOR APPLICATION NUMBER: US 60/431,143
: PRIOR FILING DATE: 2002-12-04
: PRIOR APPLICATION NUMBER: US 60/431,206
: PRIOR FILING DATE: 2002-12-04
: NUMBER OF SEQ ID NOS: 259
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 10
: LENGTH: 1956
: TYPE: DNA
: ORGANISM: Homo sapien
US-10-537-121-10

Query Match 75.5%; Score 1106.4; DB 6; Length 1956;
Best Local Similarity 99.7%; Pred. No. 1, le-199;
Matches 1119; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
Oy 144 AGATAGGCAAGAGATGGAACCAACATGGAAGTCTTCAAGTCTTCTTTATTC 403
Db 97 AGATAGGCAAGAGATGGAACCAACATGGAAGTCTTCAAGTCTTCTTTATTC 156
Oy 404 ACTTCTGATCAGCTGCTGCTTGAATTTGGAACATATTTTACAGATATTTCAATA 463
Db 157 ACTTCTGATCAGCTGCTGCTTGAATTTGGAACATATTTTACAGATATTTCAATA 216
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http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089420&ItemName=20070202_145122_us-10-753-267-19.t... 28/07

Oy	464	TTCTTATGATGGGAGATGCGATGATTTCTTTGGGAGATGCTTGCTT	523
Ds	217	TTCTTATGATGGGAGATGCGATGATTTCTTTGGGAGATGCTTGCTT	276
Oy	524	GTGCACTGATGAGATGATGCTGATTTCTGATAGACTCTACACACAGAGAA	583
Ds	277	GTGCACTGATGAGATGATGCTGATTTCTGATAGACTCTACACACAGAGAA	336
Oy	584	TATACAT	643
Ds	337	TATACAT	396
Oy	644	ATATAGACATGCTTGGAGACATATCTTGGACATGATTTTATGATGAGATG	703
Ds	397	ATATAGACATGCTTGGAGACATATCTTGGACATGATTTTATGATGAGATG	456
Oy	704	TTTGTGTGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	763
Ds	457	TTTGTGTGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	516
Oy	764	TTGATGCTATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	823
Ds	517	TTGATGCTATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	576
Oy	824	CTGGTCTTGGGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	883
Ds	577	CTGGTCTTGGGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	636
Oy	884	TTGATGCTATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	943
Ds	637	TTGATGCTATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	696
Oy	944	GGAGAGATTTGGAGAGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	1003
Ds	697	GGAGAGATTTGGAGAGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	756
Oy	1004	CTTGTCTGATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	1063
Ds	757	CTTGTCTGATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	816
Oy	1064	CTTGTCTGATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	1123
Ds	817	CTTGTCTGATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	876

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089420&ItemName=20070202_145122_us-10-753-267-19.r... 28/07

2	PRIOR FILING DATE: 2004-11-03		
2	PRIOR APPLICATION NUMBER: EP 04105485.9		
2	PRIOR FILING DATE: 2004-11-03		
2	PRIOR APPLICATION NUMBER: EP 04105484.2		
2	PRIOR FILING DATE: 2004-11-03		
2	PRIOR APPLICATION NUMBER: US 60/662,276		
2	PRIOR FILING DATE: 2005-03-14		
2	PRIOR APPLICATION NUMBER: US 60/760,293		
2	PRIOR FILING DATE: 2005-07-18		
2	NUMBER OF SEQ ID NOS: 483996		
2	SOFTWARE: PatentIn version 3.3		
2	SEQ ID NO 185216		
2	LENGTH: 1813		
2	TYPE: DNA		
2	ORGANISM: Homo Sapiens		
2	FEATURES:		
2	NAME/KEY: misc_feature		
2	LOCATION: (108)..(1107)		
2	OTHER INFORMATION: n is a, c, g, or t		
2	FEATURE:		
2	NAME/KEY: misc_feature		
2	LOCATION: (1130)..(1365)		
2	OTHER INFORMATION: n is a, c, g, or t		
US-11-266-748A-185216			
Query Match			
Best Local Similarity 97.61; P-adj. No. 2.5e-189;			
Matches 1055; Conservative 0; Mismatches 26; Indels 0; Gaps 0;			
Oy	344	AGATATAGGAGAGATGAGAGATGATTTCTTGGGATGCTGATTTTATGAGAACTA	403
Ds	49	AGATATAGGAGAGATGAGAGATGATTTCTTGGGATGCTGATTTTATGAGAACTA	108
Oy	404	ACTTGTCTGATGATGATTTTCTTGGGATGCTGATTTTATGAGAACTATTCATTA	463
Ds	109	ACTTGTCTGATGATGATTTTCTTGGGATGCTGATTTTATGAGAACTATTCATTA	168
Oy	464	TTGCTTATGATTTGGGAGAGATGCGAGATGATTTCTTTGGCAGATGCTTGGTT	523
Ds	169	TTGCTTATGATTTGGGAGAGATGCGAGATGATTTCTTTGGCAGATGCTTGGTT	228
Oy	524	GTGCACTGTGAGATACATTTGGCATATTTTCTGATAGACTCTACACAGAGAA	583
Ds	229	GTGCACTGTGAGATACATTTTGGGATGCTGATTTTCTTGGGATGCTGATTTTATGAGAACTA	288

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089420&ItemName=20070202_145122_us-10-753-267-19.r... 28/07

Oy	1124	GACTTTTCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT	1183
Ds	877	GACTTTTCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT	936
Oy	1184	AGTACAGTTTCTGAGAGATTTTAAAGACATGTTCTTGAAGTCTTGAAGAGTTT	1243
Ds	937	AGTACAGTTTCTGAGAGATTTTAAAGACATGTTCTTGAAGTCTTGAAGAGTTT	996
Oy	1244	GGATACAGATGATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	1303
Ds	997	GGATACAGATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	1056
Oy	1304	CATTGGGCTTTAAATCTTTAGATATATAGTGTCTTCTGAGAACTTCTTGAAGTGG	1363
Ds	1057	CATTGGGCTTTAAATCTTTAGATATATAGTGTCTTCTGAGAACTTCTTGAAGTGG	1116
Oy	1364	TATTGGGCTTTAAATCTTTAGATATATAGTGTCTTCTGAGAACTTCTTGAAGTGG	1423
Ds	1117	TATTGGGCTTTAAATCTTTAGATATATAGTGTCTTCTGAGAACTTCTTGAAGTGG	1174
Oy	1424	TCTCTTGGGCTTTAAATCTTTAGATATATAGTGTCTTCTGAGAACTTCTTGAAGTGG	1483
Ds	1175	TCTCTTGGGCTTTAAATCTTTAGATATATAGTGTCTTCTGAGAACTTCTTGAAGTGG	1216

RESULT 5
US-11-266-748A-185216
2 Sequence 185216, Application US/11266748A
2 Publication No. US20060194663A1
2 GENERAL INFORMATION:
2 APPLICANT: Hoffmann-La Roche
2 INVENTOR: Mulligen, Karl
2 TITLE OF INVENTION: Transcription Microarray Technology and
2 TITLE OF INVENTION: Methods of Using the Same
2 CURRENT APPLICATION NUMBER: US/11/266,748A
2 CURRENT FILING DATE: 2005-11-03 (319189)
2 PRIOR APPLICATION NUMBER: EP 04105479.2
2 PRIOR FILING DATE: 2004-11-03
2 PRIOR APPLICATION NUMBER: EP 04105482.6
2 PRIOR FILING DATE: 2004-11-03
2 PRIOR APPLICATION NUMBER: EP 04105483.4
2 PRIOR FILING DATE: 2004-11-03
2 PRIOR APPLICATION NUMBER: EP 04105507.0

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089420&ItemName=20070202_145122_us-10-753-267-19.r... 28/07

Oy	584	TATACAGTATATCATTAAGTCTGATGATTTCTTGGGATGCTGATTTTATGAGAACTA	643
Ds	289	TATACAGTATATCATTAAGTCTGATGATTTCTTGGGATGCTGATTTTATGAGAACTA	346
Oy	644	ATATGACATGCTTTGGAGATGATTTCTTGGGATGCTGATTTTATGAGAACTA	703
Ds	349	ATATGACATGCTTTGGAGATGATTTCTTGGGATGCTGATTTTATGAGAACTA	408
Oy	704	TTTGTGTGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	763
Ds	409	TTTGTGTGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	468
Oy	764	TTGATGCTATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	823
Ds	469	TTGATGCTATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	528
Oy	824	CTGGTCTTGGGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	883
Ds	529	CTGGTCTTGGGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	588
Oy	884	TTGATGCTATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	943
Ds	589	TTGATGCTATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	648
Oy	944	GGAGAGATTTGGAGAGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	1003
Ds	649	GGAGAGATTTGGAGAGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	708
Oy	1004	CTTGTCTGATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	1063
Ds	709	CTTGTCTGATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	768
Oy	1064	CTTGTCTGATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	1123
Ds	769	CTTGTCTGATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	828
Oy	1124	GACTTTTCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT	1183
Ds	829	GACTTTTCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT	888
Oy	1184	AGTACAGTTTCTGAGAGATTTTAAAGACATGTTCTTGAAGTCTTGAAGAGTTT	1243
Ds	889	AGTACAGTTTCTGAGAGATTTTAAAGACATGTTCTTGAAGTCTTGAAGAGTTT	948
Oy	1244	GGATACAGATGATGATGATTTCTTCTTGGGATGCTGATTTTATGAGAACTA	1303

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089420&ItemName=20070202_145122_us-10-753-267-19.r... 28/07


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Oy 901 ATTTTGGAGAGAGCTCTGATATATGCTCTATGATATGAAAGGAGAGTTTGAGAA 960
Db 901 ATTTTGGAGAGCTCTGATATATGCTCTATGATATGAAAGGAGAGTTTGAGAA 960
Oy 961 AGACTGGAATATATCTCAGTAAAGCTTCTGAAAGATAAAGCTTTCTGATTCAG 1020
Db 961 AGACTGGAATATATCTCAGTAAAGCTTCTGAAAGATAAAGCTTTCTGATTCAG 1020
Oy 1021 AAGTAGAGTACATGCTCTGAGAGAGAGAAATAGAGATGCTGCTGCTAGAG 1080
Db 1021 AAGTAGAGTACATGCTCTGAGAGAGAGAAATAGAGATGCTGCTGCTAGAG 1080
Oy 1081 TGATTAAGAGAGATATAGAGCTTTATAGCTCTGAGTGGAGATTTTCTACTTTA 1140
Db 1081 TGATTAAGAGAGATATAGAGCTTTATAGCTCTGAGTGGAGATTTTCTACTTTA 1140
Oy 1141 CTAAGAGCTCTATATATGAGATATATATATATATATATATATATATATAT 1200
Db 1141 CTAAGAGCTCTATATATGAGATATATATATATATATATATATATATATAT 1200
Oy 1201 GAAGTTTAAAGAGAGATTTCTTAAAGCTTGAAGAGTTTGAATATAGATATTA 1260
Db 1201 GAAGTTTAAAGAGAGATTTCTTAAAGCTTGAAGAGTTTGAATATAGATATTA 1260
Oy 1261 ATCTATGCTTTCTTCTGAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 1261 ATCTATGCTTTCTTCTGAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Oy 1321 TTTTATATATATCTGCTATATGAGAAATTTCTTATAGTATGCTTATATTTA 1380
Db 1321 TTTTATATATATCTGCTATATGAGAAATTTCTTATAGTATGCTTATATTTA 1380
Oy 1381 ACTTTTATATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 ACTTTTATATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Oy 1441 TGCTGGAGAGAGCTCTGAGCTCTGCT 1465
Db 1439 TGCTGGAGAGAGCTCTGAGCTCTGCT 1463

RESULT 3
US-10-784-004-529
: Sequence 529, Application US/10784004
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Db 361 TGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Oy 421 CGTTTATGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 CGTTTATGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Oy 481 AGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 AGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Oy 541 ACTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
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Oy 601 AAGTCTCATGAGTTTGAAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 AAGTCTCATGAGTTTGAAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Oy 661 GAGACTATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 GAGACTATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Oy 721 ATCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 ATCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Oy 781 TATGATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 TATGATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Oy 841 GATTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 GATTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Oy 901 ATTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
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Oy 961 AAGTAGATTAATATCTGAGTAAAGCTTCTGAAAGATTAAGCTTTCTGATTCAG 1020
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Db 1021 AAGTAGAGTAAATGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
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: Publication No. US20060084066A1
: GENERAL INFORMATION:
: APPLICANT: Schering-Plough Inc.
: TITLE OF INVENTION: Surrogate Markers of Pain
: FILE REFERENCE: 08201-6029-00000
: CURRENT APPLICATION NUMBER: US/10784,004
: PRIORITY FILING DATE: 2004-03-20
: NUMBER OF SEQ ID NOS: 1251
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO: 529
: LENGTH: 1741
: TYPE: DNA
: ORGANISM: human
US-10-784-004-529

Query Match 98.81; Score 1447.8; DB 12; Length 1741;
Similarity 98.11; Percent Match 98.11;
Matches 1461; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Oy 1 TTGGAGACCTGGCGAGTCTCGGTGCTGGTGGCGGCACTCATCTCGCGCGCTTCGA 60
Db 1 TTGGAGACCTGGCGAGTCTCGGTGCTGGTGGCGGCACTCATCTCGCGCGCTTCGA 60
Oy 61 ATTATAGGCTCTGGAGAGATTTGAAAATGGGAGAGAGAGAGAGAGAGAGAGAG 120
Db 61 ATTATAGGCTCTGGAGAGATTTGAAAATGGGAGAGAGAGAGAGAGAGAGAGAG 120
Oy 121 AGTTCAAGCTCTGGCTGGAGATATGATATCACTTTTACCTGAGATCTCTGCA 180
Db 121 AGTTCAAGCTCTGGCTGGAGATATGATATCACTTTTACCTGAGATCTCTGCA 180
Oy 181 GAGCACTTAATAATGCTGGAGATATGATATCACTTTTACCTGAGATCTCTGCA 240
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Oy 241 ACATGGGAGCTCTTATAGTATCATGAGCCCTTATCTTCTTCTTACCTGGATT 300
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Oy 301 TTATTCATTAATTAACCTTATATGAAAATACAAATTCAAAGGATAGCCAGACA 360
Db 301 TTATTCATTAATTAACCTTATATGAAAATACAAATTCAAAGGATAGCCAGACA 360
Oy 361 TGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 TGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

RESULT 4
US-10-784-107-3400
: Sequence 3400, Application US/0988107
: Patent No. US20020142981A1
: GENERAL INFORMATION:
: APPLICANT: Vockley, Joseph G.
: APPLICANT: Schering-Plough Inc.
: APPLICANT: Genentech, Inc.
: FILE REFERENCE: 44921-5028-WO
: CURRENT APPLICATION NUMBER: US/09/880,107
: PRIORITY FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: US 60/211,379
: PRIORITY FILING DATE: 2000-06-14
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Oy 1141 CCTACAGTCTTATATATGAGAAATATATATATATATATATATATATATATAT 1200
Db 1141 CCTACAGTCTTATATATGAGAAATATATATATATATATATATATATATATAT 1200
Oy 1201 GAGCTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
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Db 1261 ATCTATGCTTTCTGCGAGTAAAGCATAGGCTGAGTTCATGCTTCTTAAATC 1320
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Db 1321 TTTTATATATATCTGCTATATGAGAAATTTCTTATAGTATGCTTATATTTA 1380
Oy 1381 ACTTTTATATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 ACTTTTATATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Oy 1441 TGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1465
Db 1439 TGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1463

RESULT 4
US-10-784-107-3400
: Sequence 3400, Application US/0988107
: Patent No. US20020142981A1
: GENERAL INFORMATION:
: APPLICANT: Vockley, Joseph G.
: APPLICANT: Schering-Plough Inc.
: APPLICANT: Genentech, Inc.
: FILE REFERENCE: 44921-5028-WO
: CURRENT APPLICATION NUMBER: US/09/880,107
: PRIORITY FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: US 60/211,379
: PRIORITY FILING DATE: 2000-06-14
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1 PRIOR APPLICATION NUMBER: US 60/237,054
2 PRIOR FILING DATE: 2005-10-02
3 NUMBER OF SEQ ID NOS: 3950
4 SOFTWARE: PatentIn Ver. 2.1
5 SEQ ID NO 3400
6 LENGTH: 1751
7 TYPE: DNA
8 ORGANISM: Homo sapiens
9 OTHER INFORMATION: Genbank Accession No. U32002014591A1 U60205
US-09-880-107-3400

Query Match 94.01; Score 1376.6; DB 3; Length 1751;
Best Local Similarity 99.61; Pred. No. 1.4e-307;
Matches 1391; Conservative 0; Mismatches 4; Indels 2; Gaps 1;
Oy 69 GCTGTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 128
Db 5 GATGCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 64
Oy 125 ATCTGCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 188
Db 65 ATCTGCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 124
Oy 189 TAAATGCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 248
Db 125 TAAATGCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 184
Oy 249 ATCTGCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 308
Db 185 ATCTGCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 244
Oy 309 ATCTGCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 368
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Db 305 CAAATGCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 364
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Oy 489 AGATGCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 548
Db 425 AGATGCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 484

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Db 1085 TTCTATATGTGAGAAATGAATATATATATATATATATATATATATATATAT 1144
Oy 1209 AAGAGACATGCTGCTGAGCTGCGAGAGATTTGAGTACTAGAGATATATATATAT 1268
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Oy 1269 CTTTCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 1328
Db 1205 CTTTCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 1264
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Oy 1389 TTATTTTTTTTGGAGAAAGCGACAACTGCTGCTGCGAGATCTTTAGTTCG 1448
Db 1325 TTATTTTTTTTGGAGAAAGCGACAACTGCTGCTGCGAGATCTTTAGTTCG 1382
Oy 1449 CAGTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1465
Db 1383 CAGTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1399

RESULT 5
US-09-546-406-5
Sequence 5, Application US/05946406
Patent No. US2002012956A1
GENERAL INFORMATION:
APPLICANT: Relley, Richard I.
INVENTOR: Grange, Dorothy K.
TITLE OF INVENTION: BIOSYNTHESIS ENZYMES
FILE REFERENCE: 20335/36435
CURRENT APPLICATION NUMBER: US/09/946,406
PRIOR FILING DATE: 2001-09-05
PRIOR FILING DATE: 2005-06-01
INVENTOR'S SEQ ID NO: 21
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 1751
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089419&ItemName=20070202_145118_us-10-753-267-19.r... 2/8/07

Db 425 AAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484
Oy 549 CTATTTTGTGATAGATCTTACACACAAAGAGATATATATATATATATATATATAT 608
Db 485 CTATTTTGTGATAGATCTTACACACAAAGAGATATATATATATATATATATATAT 544
Oy 609 TCATGATTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
Db 545 TCATGATTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 604
Oy 669 AATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
Db 605 AATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 664
Oy 729 TTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788
Db 725 TTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 724
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Oy 909 AACAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 968
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Db 1145 TTCTATATGTGAGAAATGAAT 1208

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1 NAME/KEY: CDS
2 LOCATION: (27)..(908)
3 US-09-546-406-5
Query Match 94.01; Score 1376.6; DB 3; Length 1751;
Best Local Similarity 99.61; Pred. No. 1.4e-307;
Matches 1391; Conservative 0; Mismatches 4; Indels 2; Gaps 1;
Oy 69 GCTGTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 128
Db 5 GATGCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 64
Oy 129 ATCTGCTGCGAGATTTGAAATGCGACAAATGAAGTGTGCGATCTTTAGTTCG 188
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Db 425 AAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484
Oy 549 CTATTTTGTGATAGATCTTACACACAAAGAGATATATATATATATATATATATATAT 608
Db 485 CTATTTTGTGATAGATCTTACACACAAAGAGATATATATATATATATATATATATAT 544
Oy 609 TCATGATTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668

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Db 545 TCTAGTCTGAGGCTGATTTGGATAGGATGATATGACATGCTTTGGAGACTCT 604
Oy 669 AATCTCTGAGACTGATTTGATAGGATGATGATGATGATGATGATGATGATGAT 728
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Oy 729 TTGGGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 788
Db 665 TTGGGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 724
Oy 789 TCTCTGAGGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 848
Db 725 TCTCTGAGGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 784
Oy 849 CCACATGACTTCTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 908
Db 785 CCACATGACTTCTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 844
Oy 909 ACAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 968
Db 845 ACAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 904
Oy 969 ATAAATATCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028
Db 905 ATAAATATCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 964
Oy 1029 AGCTAGATGCTTCTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1088
Db 965 AGCTAGATGCTTCTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1024
Oy 1089 AGAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1148
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Db 1085 TCTATATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1144
Oy 1209 AAGAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1268
Db 1145 AAGAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1204
Oy 1269 CTTTCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1328
Db 1205 CTTTCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1264

2 PRIOR APPLICATION NUMBER: 60/373,061
2 PRIOR FILING DATE: 2002-04-19
2 PRIOR FILING DATE: 2002-04-19
2 PRIOR FILING DATE: 2002-04-19
2 PRIOR APPLICATION NUMBER: 60/373,061
2 PRIOR FILING DATE: 2002-06-12
2 PRIOR APPLICATION NUMBER: 60/390,971
2 PRIOR FILING DATE: 2002-06-24
2 PRIOR APPLICATION NUMBER: 60/394,130
2 PRIOR FILING DATE: 2002-07-03
2 PRIOR APPLICATION NUMBER: 60/394,130
2 PRIOR FILING DATE: 2002-07-10
2 PRIOR APPLICATION NUMBER: 60/404,904
2 PRIOR FILING DATE: 2002-08-21
2 PRIOR APPLICATION NUMBER: 60/405,450
2 PRIOR FILING DATE: 2002-08-23
2 Remaining Prior Application data removed - See File Wrapper or PALM.
2 REMAINING PRIOR APPLICATION NUMBER: 60/405,450
2 REMAINING PRIOR APPLICATION NUMBER: 60/405,450
2 SEQ ID NO 3
2 LENGTH: 1751
2 TYPE: DNA
2 ORGANISM: Homo Sapiens
us-10-353-690-3
Query Match
Best Local Similarity 99.61; Pred. No. 1-4e-307;
Matches 1391; Conservative 0; Mismatches 4; Indels 2; Gaps 1;
Oy 69 GCTCTGAGAGATTTGAAATGAGGATGATGATGATGATGATGATGATGATGAT 128
Db 5 GATGATGAGAGATTTGAAATGAGGATGATGATGATGATGATGATGATGATGAT 64
Oy 129 ATCTCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 188
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Oy 249 ATCTCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 308
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Oy 1449 CAGTCTGAGCTGATGCT 1465
Db 1383 CAGTCTGAGCTGATGCT 1399
RESULT 6
us-10-353-690-3
2 Sequence 3, Application US/10353690
2 Publication No. US20030215840A1
2 GENERAL INFORMATION:
2 APPLICANT: Logan, Thomas Joseph
2 APPLICANT: Chun, Myoung
2 APPLICANT: Galvin, Katherine H.
2 APPLICANT: Reilly, Aileen
2 APPLICANT: Anderson, David L.
2 APPLICANT: Donoghue, Mary
2 APPLICANT: Stagliano, Nancy
2 APPLICANT: Perodine, Jacquelin
2 APPLICANT: Rodriguez-Way, Amelie
2 TITLE OF INVENTION: Methods and compositions for treating
2 TITLE OF INVENTION: Cardiovascular diseases using 102, 6169, 6183, 7371, 14385,
2 TITLE OF INVENTION: 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550,
2 TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 10036, 16105, 38550,
2 TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
2 TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
2 TITLE OF INVENTION: 283, 2534, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
2 TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
2 TITLE OF INVENTION: 9792, 15400, 1452 of 6585 molecules
2 THE REFERENCE: PRIOR INFORMATION:
2 CURRENT FILING DATE: 2003-01-29
2 PRIOR APPLICATION NUMBER: 60/353,224
2 PRIOR FILING DATE: 2002-02-01
2 PRIOR APPLICATION NUMBER: 60/364,529
2 PRIOR FILING DATE: 2002-03-15

Oy 309 ATTATAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 368
Db 245 ATTATAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 304
Oy 369 CCAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 428
Db 305 CCAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 364
Oy 429 TTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 488
Db 365 TTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 424
Oy 489 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 548
Db 425 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
Oy 549 CTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 608
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Oy 609 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 668
Db 545 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 604
Oy 669 AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 728
Db 605 AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
Oy 729 TTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 788
Db 665 TTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 724
Oy 789 TCTCTGAGGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 848
Db 725 TCTCTGAGGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 784
Oy 849 CCACATGACTTCTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 908
Db 785 CCACATGACTTCTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 844
Oy 909 ACAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 968
Db 845 ACAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 904
Oy 969 ATAAATATCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028

905	ATAAATATCTCAAGCTAAGCTCTCGAGAAATAAAGCTTTTCTCGAATCGAGAACTAGT	954
1029	AGCTACATATGCTTTGGAGAGAGAAATAGCACTGCTCTGGCTACTACTAGTGATAAA	1088
965	AGCTACATATGCTTTGGAGAGAGAAATAGCACTGCTCTGGCTACTACTAGTGATAAA	1024
1089	AGACATATACAGAGCTTATTAAGCTCTGATGCGAGAGCTTTCTCTACTACTACAG	1148
1025	AGACATATACAGAGCTTATTAAGCTCTGATGCGAGAGCTTTCTCTACTACTACAG	1084
1149	TCCTATATATGTAGAAATAGATAAATATATATTAAGCTACAGTTCATCGAGGAAGTTTT	1208
1085	TCCTATATATGTAGAAATAGATAAATATTAAGCTACAGTTCATCGAGGAAGTTTT	1144
1209	AAAGAGCATATGCTCTAGCTCTCAGAGAGGTTTGGATACAGATAGATTAATCTATGG	1268
1145	AAAGAGCATATGCTCTAGCTCTCAGAGAGGTTTGGATACAGATAGATTAATCTATGG	1204
1269	CTTTTCTCCGATATAAACCATAGCGCTGAGGTCACATTTGGGCTTTTAAATCTTTAGAT	1328
1205	CTTTTCTCCGATATAAACCATAGCGCTGAGGTCACATTTGGGCTTTTAAATCTTTAGAT	1264
1329	ATATATGCTGCAATTCAGAAATCTCTCATAGTGGAATTTGGCTATTAATTACTTTTTT	1388
1265	ATATATGCTGCAATTCAGAAATCTCTCATAGTGGAATTTGGCTATTAATTACTTTTTT	1324
1389	TTATATTTTTTTTTTGAGACAAAGCCAAACACTCTGCTCTGGCTGGAGTGCGTGCCA	1448
1325	TTATATTTTTTTTTTGAGACAAAGCCAAACACTCTGCTCTGGCTGGAGTGCGTGCCA	1382
1449	CAGCTCTAGCTCACTGC	1465
1383	CAGCTCTAGCTCACTGC	1399

RESULT 7
US-10-240-425-1419
; Sequence 1419, Application US/10240425
; Publication No. US20040033502A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris

http://es/ScoreAccessWeb/GetItem.action?AppId=10753267&seqId=1089419&itemName=20070202_145118_us-10-753-267-19.r... 2/8/07

SCORE Search Results Details for Application 10753267 and Search Result 20070202 145118 us-10-753-267-19.mpbm.

[illegible]

MAIL ORDER

? APPLICANT: Wetzel, Jon C.
 ? APPLICANT: Schreff, Uwe
 ? APPLICANT: Voelckley, Joseph G.
 ? TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
 ? FILE REFERENCE: 44921-5026
 ? CURRENT APPLICATION NUMBER: US/10/240,425
 ? PRIOR FILING DATE: 2002-09-30
 ? PRIOR APPLICATION NUMBER: PCT/US01/09847
 ? PRIOR PUBLICATION NUMBER: US 60/193,446
 ? PRIOR FILING DATE: 2000-03-31
 ? NUMBER OF SEQ ID NOS: 1588
 ? SOFTWARE: Patent In Ver. 2.1
 ? SEQ ID NO 1449
 ? LENGTH: 1751
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 ? EXTRACT:
 ? OF: 240-425-1449
 ? INFORMATION: Genbank Accession No. U53004003302A1 U60205
 ? US-10-240-425-1449

Query Match	94.0%	Score 1376.61	DB 8:	Length 1751:
Best Local Similarity	99.61%	Prod. No. 1.4e+307		
Matches 1391:	Conservative 0:	Mismatches 4:	Indels 2:	Gaps 1:
Oy	69	GTCTGTCTGCGAGATTGGAAATGGCGAAGATGAAGTCTGAGCTTTATTGCGC	128	
Oy	111	TTTTTTTCTGCGAGATTTGGAAATGGCGAAGATGAAGTCTGAGCTTTATTGCGC	188	
Dy	5	GTATCTGCGAGATTTGGAAATGGCGAAGATGAAGTCTGAGCTTTATTGCGC	64	
Oy	129	ATCTGTGCTGTGGATTTGTAGTACCTTTACCTGAGATCTCTCTGCGAGACANT	177	
Dy	65	ATCTGTGCTGTGGATTTGTAGTACCTTTACCTGAGATCTCTCTGCGAGACANT	124	
Oy	189	TAAATTCCTTGAGACTATGTGTGATTAATATACAAATGTCGATTCGACATGGG	246	
Dy	125	TAAATTCCTTGAGACTATGTGTGATTAATATACAAATGTCGATTCGACATGGG	184	
Oy	249	ATCCCTTTATAGTCTGAGAGCCTTTATTTCTTATCTGTCTACTGGATTTTTATTCA	308	
Oy	185	ATCCCTTTATAGTCTGAGAGCCTTTATTTCTTATCTGTCTACTGGATTTTTATTCA	244	
Oy	309	ATTATCTCTATATGTCGAGAGCCTTTATTTCTTATCTGTCTACTGGATTTTTATTCA	368	
Oy	245	ATTATCTCTATATGTCGAGAGCCTTTATTTCTTATCTGTCTACTGGATTTTTATTCA	304	

http://es/ScoreAccessWeb/GetItem.action?Appld=10753267&seqId=1089419&itemName=20070202_145118_us-10-753-267-19.r... 2/8/07

Db	905	ATAAATATCTCAAGCTAAGCTCTCTGAGAAATAAAGCTTTTCTCGAATCTAGAACTACT	954
Oy	1029	AGCTACATATGCTTTGGAGAGAGAAATAGCACTCTCTCTGGCTACTACTAGTGATAAA	1088
Db	965	AGCTACATATGCTTTGGAGAGAGAAATAGCAATGCTCTCTGGCTACTACTAGTGATAAA	1024
Oy	11089	AGACATATACAGACTTTAATTAAGCTCTCTGAGAGCTTTCTCTTAATCTACCTACAG	1148
Db	1025	AGACATATACAGACTTTAATTAAGCTCTCTGAGAGCTTTCTCTTAATCTACCTACAG	1084
Oy	11149	TTCTATATATGTAGAAATAGATAAATAATATATTAAGTACAGATGTTCTCATAGGAAGTTTT	1208
Db	1085	TTCTATATATGTAGAAATATCAATATATTAATTAAGTACAGATGTTCTCATAGGAAGTTTT	1144
Oy	11145	AAAGACCATATGCTCTAGCTCTCAAGAGGTTTGGATACAGATGATTAATCTATGG	1268
Db	1145	AAAGACCATATGCTCTAGCTCTCAAGAGGTTTGGATACAGATGATTAATCTATGG	1204
Oy	1269	CTTTTCTCCAGTAAACACATAGCGCTGAGGTCACATTTGGGCTTTAAATCTTTTAGAT	1328
Db	1205	CTTTTCTCCAGTAAACACATAGCGCTGAGGTCACATTTGGGCTTTAAATCTTTTAGAT	1264
Oy	1329	ATATATGCTGCAATTCAGAAATCTCTCAATAGTGGAATTTGGCTATTAATTACTTTTTT	1388
Db	1265	ATATATGCTGCAATTCAGAAATCTCTCAATAGTGGAATTTGGCTATTAATTACTTTTTT	1324
Oy	1389	TTATATTTTTTTTTTGAGACAAAGCCAAACACTCTCTCTCTGGCTGGAGTGCGTGCCA	1448
Db	1225	TTATATTTTTTTTTTGAGACAAAGCCAAACACTCTCTCTCTGGCTGGAGTGCGTGCCA	1382
Oy	1449	CAGCTCTAGCTCACTGC	1465
Db	1383	CAGCTCTAGCTCACTGC	1399

RESULT 7
US-10-240-425-1419
; Sequence 1419, Application US/10240425
; Publication No. US20040033502A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris

http://es/ScoreAccessWeb/GetItem.action?AppId=10753267&seqId=1089419&itemName=20070202_145118_us-10-753-267-19.r... 2/8/07

SCORE Search Results Details for Application 10753267 and Search Result 20070202 145118 us-10-753-267-19.mpbm.

[illegible]

MAIL ORDER

? APPLICANT: Wetzel, Jon C.
 ? APPLICANT: Schreff, Uwe
 ? APPLICANT: Voelckley, Joseph G.
 ? TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
 ? FILE REFERENCE: 44921-5026
 ? CURRENT APPLICATION NUMBER: US/10/240,425
 ? PRIOR FILING DATE: 2002-09-30
 ? PRIOR APPLICATION NUMBER: PCT/US01/09847
 ? PRIOR PUBLICATION NUMBER: US 60/193,446
 ? PRIOR FILING DATE: 2000-03-31
 ? NUMBER OF SEQ ID NOS: 1588
 ? SOFTWARE: Patent In Ver. 2.1
 ? SEQ ID NO 1449
 ? LENGTH: 1751
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 ? EXTRACT:
 ? OF: 240-425-1449
 ? INFORMATION: Genbank Accession No. U53004003302A1 U60205
 ? US-10-240-425-1449

Query Match	94.0%	Score 1376.61	DB 8:	Length 1751:
Best Local Similarity	99.6%:	Prod. No. 1.4e+307		
Matches 1391:	Conservative 0:	Mismatches 4:	Indels 2:	Gaps 1:
Oy	69	CTCTCTCTCGAGAGATTGGAAATGGCGAAGATGAAGTCTGAGCATTCTTATTCGCG	128	
Oy	111	TT		
Oy	5	ATACATCTCGAGAAATTTGGAAATGGCGAAGATGAAGTCTGAGCATTCTTATTCGCG	64	
Dy	129	ATCTCTGCTGTGGATATGTAGATCACTTTTACCTGAGATCTCTCTCGAGACAGCTT	188	
Dy	65	ATCTCTGCTGTGGATATGTAGATCACTTTTACCTGAGATCTCTCTCGAGACAGCTT	124	
Oy	189	TAAATCTCTTGAGACTATGTGTGATTAATATACAAATCTCGATTCGACATGGCG	248	
Dy	125	TAAATCTCTTGAGACTATGTGTGATTAATATACAAATCTCGATTCGACATGGCG	184	
Oy	249	ATCTCTTTATAGTCTGAGACGCTTTATTTCTTATCTCTGCTACTGATTTTTATTCCA	308	
Oy	185	ATCTCTTTATAGTCTGAGACGCTTTATTTCTTATCTCTGCTACTGATTTTTATTCCA	244	
Oy	309	ATTATCTCTTATGATTCGAGACGCTTTATTTCTTATCTCTGCTACTGATTTTTATTCCA	368	
Oy	245	ATTATCTCTTATGATTCGAGACGCTTTATTTCTTATCTCTGCTACTGATTTTTATTCCA	304	

http://es/ScoreAccessWeb/GetItem.action?Appld=10753267&seqId=1089419&itemName=20070202_145118_us-10-753-267-19.r... 2/8/07

669	ANTCTCTGGACGGGATTTTCATGGGATCGCTCTTTCTGGATCATCATGATCTCTCT	721
Dib		
665	ANTCTCTGGACCGGATTTTCATGGGATCGCTCTTTCTGGATCATCATGATCTCTCT	664
Dib		
725	TGGGCGATGGGATGACATCTGGTTATTATGAAACCTATGATATCGATACGGTATGATAT	788
Oy		
725	TGGGCGATGGGATGACATCTGGTTATTATGAAACCTATGATATCGATACGGTATGATAT	724
Oy		
789	TGCTCTCAAGCGCTTAATCTGATCGCTCTTTCTCTGCGTCTGGGATCATGATATTCGA	848
Oy		
725	TTCTCTCTCAAGCGCTTAATCTGATCGCTCTTTCTCTGCGTCTGGGATCATGATATTCGA	788
Dib		
849	CCAGCATGACCTTTCAATGGGAATATCTCTCAGCATTTACATGGTGGGATGAATTTTGG	908
Oy		
785	CCAGCATGACCTTTCAATGGGAATATCTCTCAGCATTTACATGGTGGGATGAATTTTGG	844
Dib		
905	ACAGCATGACCTTTCAATGGGAATATCTCTCAGCATTTACATGGGAAGGATGACCTCA	968
Oy		
905	ACAGCATGACCTTTCAATGGGAATATCTCTCAGCATTTACATGGGAAGGATGACCTCA	904
Oy		
969	ATAATATCTCATGATGAAGCTCTCGAGAGATAAGCTTTCTCTGATTCAGAAAGTACT	1028
Oy		
905	ATAATATCTCATGATGAAGCTCTCGAGAGATAAGCTTTCTCTGATTCAGAAAGTACT	964
Dib		
1029	AGCTACATATCTCTCTGGAGAGAAATACGATCTCTCTGGCTACTACGTGTATATAA	1088
Oy		
985	AGCTACATATCTCTCTGGAGAGAAATACGATCTCTCTGGCTACTACGTGTATATAA	1024
Dib		
1089	AGACATATACAGCTTTACAGCTCTGGGAGATTTCTCTACTACCTACAGTACAG	1148
Oy		
1025	AGACATATACAGCTTTACAGCTCTGGGAGATTTCTCTACTACCTACAGTACAG	1084
Dib		
1149	TCTATATATCTAGAAATGAATATATATTTAGTACAGTTTCTCATGGAGAGTTT	1208
Oy		
1085	TCTATATATCTAGAAATGAATATATTTAGTACAGTTTCTCATGGAGAGTTT	1144
Dib		
1209	AAAGACATATCTCTAGCTCTCAGAGAGTTTGGATATACAGAGTATATATCTATGG	1268
Oy		
1149	AAAGACATATCTCTAGCTCTCAGAGAGTTTGGATATACAGAGTATATATCTATGG	1204
Dib		
1269	CTTTTCTCCGAGTAAACCATGCGCTGACATCTATGGCTCTTAATCTCTTTAGAT	1328
Oy		
1205	CTTTTCTCCGAGTAAACCATGCGCTGAGTCTACATCTGGGCTCTTAATCTCTTTAGAT	1264
Dib		

http://es/ScoreAccessWeb/GetItem.action?Appld=10753267&seqId=1089416&ItemName=20070202_145106_us-10-753-267-19.r... 2/8/07

SCORE Search Results Details for Application 10753267 and Search Result 20070202_145108_

US-09-513-999C-1161

Query Match 29.7A; score 435.6; DB 3; Length 474;
 Best Local Similarity 99.81; Pred. No. 2, 7e-97;
 Matches 435; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY	1	TTGGACACCTGGAGTCTGTGTGTGGTGGCGGACATCTCGCGCGCTGCA	60
DB			
OY	39	TTGGACACCTGGAGTCTGTGTGTGGTGGCGGACATCTCGCGCGCTGCA	98
DB			
OY	61	ATATATAGGCTGTGCAAGATTGAAATATGGCAACAATGAAGTGTACATCTT	120
DB			
OY	99	ATATATAGGCTGTGCAAGATTGAAATATGGCAACAATGAAGTGTACATCTT	158
DB			
OY	121	AGTTGACATCTTGGCTGTGGATTATGATATCACTTTACTTGTAGATCTCTGCA	180
DB			
OY	159	ATGACATCTTGGCTGTGGATTATGATATCACTTTACTTGTAGATCTCTGCA	218
DB			
OY	181	GACATCTTAAAAATGCTTGGCACTATATGATATATATACAAAGTGTGAGATGCA	240
DB			
OY	219	GACATCTTAAAAATGCTTGGCACTATATGATATATATACAAAGTGTGAGATGCA	278
DB			
OY	241	ACATGGGATGCTTATATGTTATGAGGCCCTTTATCTTATCTGTGTACTGGATT	300
DB			
OY	279	ACATGGGATGCTTATATGTTATGAGGCCCTTTATCTTATCTGTGTACTGGATT	338
DB			
OY	301	TATTTTCATTTATGCTTATATGAAATATGAATATCAAGAGTATGCGACGACA	360
DB			
OY	339	TATTTTCATTTATGCTTATATGAAATATGAATATCAAGAGTATGCGACGACA	398
DB			
OY	361	TGGGAAACGATGGAGTGTTCGAAGTGTCTCTTTATGCTGTATGTCAGCTG	420
DB			
OY	399	TGGGAAACGATGGAGTGTTCGAAGTGTCTCTTTATGCTGTATGTCAGCTG	458
DB			
OY	421	CTTTTGATTTGGGAA	436
DB			
OY	459	CTTTTGATTTGGGAA	474
DB			

RESULT 3
US-09-248-796A-3847
: Sequence 3847, Application US/09248796A
: Patent No. 6747137
: GENERAL INFORMATION:
: APPLICANT: Keith Weinstock et al

http://es/ScoreAccessWeb/GetItem.action?AppId=10753267&seqId=1089416&itemName=20070202_145106_us-10-753-267-19_1... 2/8/17

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Oy 1329 MYATCTGCTCAATTCAGAAATCTCTTCAGATGGTATTCGGCTCTATATTACTTTTT 1334
Db 1265 ATATCTGCTCAATTCAGAAATCTCTTCAGATGGTATTCGGCTCTATATTACTTTTT 1324
Oy 1389 TTTATTTTTTTTGGAGACAGCCAGCAACTCTGCTCTGGCTGAGCTGGTGCCA 1448
Db 1325 TTTATTTTTTTTGGAGACAGCCAGCAACTCTGCTCTGGCTGAGCTGGTGCCA 1382
Oy 1449 CAGCTCAGCTCAGCTGCTC 1465
Db 1383 CAGCTCAGCTCAGCTGCTC 1399

RESULT 2
US-09-513-999C-1161
Patent No. 6781961 Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59,032,REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1995-02-26
NAME OF THE INVENTOR: Dumas Milne Edwards, J.B.
SOFTWARE: SEQ ID NO 1161
LENGTH: 474
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: CDS
LOCATION: 129..473
FEATURE:
NAME/KEY: miac feature
LOCATION: 353
OTHER INFORMATION: seq or g
NAME:
NAME: UNSURE
LOCATION: 75
OTHER INFORMATION: Xaa-ile or Met

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<http://es.ScoreAccessWeb/CellItem.action?AppId=10753267&seqId=1089416&ItemName=20070202> 145106 us-10-753-267-19.r... 2/8/07

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SCORE Search Results Details for Application 10753267 and Search Result 20070202_1451006

? TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA
? TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
? FILE REFERENCE: 107196.132
? CURRENT APPLICATION NUMBER: US/09/248,796A
? CURRENT FILING DATE: 1999-02-12
? PRIOR APPLICATION NUMBER: US 60/074,725
? PRIOR FILING DATE: 1998-02-13
? PRIORITY CLAIMED FROM: US 60/096,409
? PRIOR FILING DATE: 1998-08-13
? NUMBER OF SEQ ID NOS: 28208
? SEQ ID NO 3847
? LENGTH: 921
? TYPE: DNA
? ORGANISM: Candida albicans
US-09-248-796A-3847

Query Match          10-11; Score 147.6; DB 3; Length 921;
Best Local Similarity 52.6%; Pred. No. 1.3e+26;
Matches 404; Conservative 0; Mismatches 34; Indels 20; Gaps 3;

Oy      187 TTAAAACTCGTGACACTATTGTGATTAATAAAAGTCCGCAT--TCGAACAT 244
Db      149 TGAAAATATGGGGCATATATATATATGCCCAATATTATCTCATTGAT 208

Oy      245 GGGAATCCCTTAGCTACAAGCCCTTTTCTCTATCTGTCTACCCTGGATTTTT 304
Db      209 TATTATTTTACTCACTAACATTTTTCATTTTGGTAGAGTTCATGGCGATTAA 268

Oy      305 TCATTTATCTCTCTATCAAAMATATGAATATGAAGAATAGCCAGAKATGGG 364
Db      268 TTGATAGATTCTCTATTTTAGAAATGGAAATTCAGATGAAAMAATCGCTATG 328

Oy      365 AAACACATGGAAGTGTTCCTCAAAAGTCTCTCTTTATCACTCTGTGTCAGCTG 424
Db      329 AACACATGGGAATCTTCAATCAATGCTTTTACGCTCTCTCTCTTAGTAGCTTC 388

Oy      425 TGATTTGTGGAACCTATTATTACAGAGATTTCATCATTTCTATTGGGAANAGA 484
Db      389 CAATTTGGTGTITTCATCCATATATGTCCAAMATTTGTTATTAGTATATCA---AGTASCAT 445

Oy      486 TCCCAAGATGGTATTCTTTTGGCAAGATCTTGGTGTGCGACATATGGAACTT 544
Db      445 CTCTCAATATCATTTGTTGTTATGTTGGAGATGTTGTTTCTTTTGGAAAGTAT 505

Oy      545 GGCACTATTTCTGCATAGACTCTACACAGCAAGATGATATAGCATAGTATCAT 604

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http://es/ScoreAccessWeb/GetItem.action?AppId=10753267&seqId=1089416&itemName=20070202 | 45106 us-10-753-267-19 | ... 2/8/07

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Db 506 GGCATATGCTTTCATAGAGATATATATGCGGTTCTCATAGATATATCATAGAC 565
Oy 605 TTGATCATGAGTTCATGAGCTTCATGAGATGAGATGAGATGAGATGAGATGAG 664
Db 566 GACATCATAGATGAGTTCATGAGCTTCATGAGATGAGATGAGATGAGATGAG 625
Oy 665 CTCATATGAGTTCATGAGCTTCATGAGATGAGATGAGATGAGATGAGATGAG 714
Db 626 TTGCTTATAGATGAGTTCATGAGCTTCATGAGATGAGATGAGATGAGATGAG 685
Oy 715 -----CATGATATGCTTCATGAGCTTCATGAGATGAGATGAGATGAGATGAG 769
Db 686 ATGCTCATATGAGTTCATGAGCTTCATGAGATGAGATGAGATGAGATGAGATGAG 745
Oy 770 TCGATATGAGTTCATGAGCTTCATGAGATGAGATGAGATGAGATGAGATGAG 829
Db 746 CTCATGCTGCTTCATGAGCTTCATGAGATGAGATGAGATGAGATGAGATGAG 805
Oy 830 CTCGCTCATATGAGTTCATGAGCTTCATGAGATGAGATGAGATGAGATGAGATGAG 889
Db 806 CTGATCATATGAGTTCATGAGCTTCATGAGATGAGATGAGATGAGATGAGATGAG 865
Oy 890 GGTGATGAGTTCATGAGCTTCATGAGATGAGATGAGATGAGATGAGATGAGATGAG 937
Db 866 GGTGATGAGTTCATGAGCTTCATGAGATGAGATGAGATGAGATGAGATGAGATGAG 913
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RESULT 4
US-09-439-554-23
: Sequence 23, Application US/09439554
: Patent No. 6479733
: GENERAL INFORMATION:
: APPLICANT: Rafalski, Jan Antoni
: APPLICANT: Odell, Joan T.
: APPLICANT: Sakai, Hajime
: INVENTOR: Knappe, Catherine J.
: APPLICANT: Knappe, Catherine J.
: APPLICANT: Farnoud, Omidyar O.
: TITLE OF INVENTION: STEROL METABOLISM ENZYMES
: FILE REFERENCE: B61114 US NA
: CURRENT APPLICATION NUMBER: US/09/439,554
: PRIOR FILING DATE: 1999-11-12
: EARLIER APPLICATION NUMBER: 60/108,351
: EARLIER FILING DATE: 1998-06-07 6479733emb4-13
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http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089416&ItemName=20070202_145106_us-10-753-267-19.t... 2/8/07

SCORE Search Results Details for Application 10753267 and Search Result 20070202_145106_us-10-753-267-19.mi. Page 11 of 23

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Db 555 TCTTGCTGCTTTCATAGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
Oy 731 GGGATGCTGAGCATATGCTTATGAGAACTATGATGCTGCTGCTGCTGCTGCTGCT 790
Db 615 GGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 674
Oy 791 CTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850
Db 675 CATGAGTCTTCCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 734
Oy 851 AC-----ATGACCTTATGAGAACTGCTTCCATGCTTCCATGCTGCTGCTGCTGCT 901
Db 735 ACCGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 794
Oy 902 TTTTTCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961
Db 795 TATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
Oy 962 AGACTG 967
Db 855 ACAGTG 860
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RESULT 5
US-09-248-796A-3848
: Sequence 3848, Application US/09248796A
: Patent No. 6747137
: GENERAL INFORMATION:
: APPLICANT: Reich, Reinhold et al
: INVENTOR: Reich, Reinhold et al
: TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
: CURRENT APPLICATION NUMBER: US/09/248,796A
: PRIOR FILING DATE: 1999-02-12
: CURRENT APPLICATION NUMBER: US 60/074,725
: PRIOR FILING DATE: 1998-02-13
: INVENTOR: Reich, Reinhold et al
: PRIOR FILING DATE: 1998-08-13
: NUMBER OF SEQ ID NOS: 28208
: SEQ ID NO 3848
: LENGTH: 969
: TYPE: DNA
: ORGANISM: Candida albicans
US-09-248-796A-3848
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http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089416&ItemName=20070202_145106_us-10-753-267-19.t... 2/8/07

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: NUMBER OF SEQ ID NOS: 30
: SEQUENCE: Microsome Office 97
: SEQ ID NO 23
: LENGTH: 1192
: TYPE: DNA
: ORGANISM: Cytidine max
US-09-439-554-23
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Query Match 8,24; Score 119.6; DB 3; Length 1192;
Best Local Similarity 49.94; P-adj No. 3, 1e-19;
Matches 392; Conservative 0; Mismatches 379; Indels 15; Gaps 3;
Oy 191 AAATGCTTGGAGTATGATGATATATATATATATATATATATATATATATATATAT 250
Db 81 AATGCTTGGAGTATGATGATATATATATATATATATATATATATATATATATATAT 140
Oy 251 GCGTATGCTGAGAGGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
Db 141 GTTCTTCTGATGAGGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 200
Oy 311 TTATGCTTATATATATATATATATATATATATATATATATATATATATATATATAT 370
Db 201 GCGGAGGCTGATGAGAGAGTACAAATTC---AGGCAAAATACAGCTGCTGCTGCTGCT 257
Oy 371 AATGAGTGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 430
Db 258 AGGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 317
Oy 431 GTGAGACTATATATATATATATATATATATATATATATATATATATATATATATATAT 490
Db 318 TTTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 377
Oy 491 GATGCTATTTCTTGGAGAGTCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
Db 378 GGAAGTGTCTAATCAATATATATATATATATATATATATATATATATATATATATAT 434
Oy 551 ATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610
Db 435 ACTGGAGATGATATATATATATATATATATATATATATATATATATATATATATATAT 494
Oy 611 ATGAGTTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 670
Db 495 ATGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 554
Oy 671 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 730
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SCORE Search Results Details for Application 10753267 and Search Result 20070202_145106_us-10-753-267-19.mi. Page 12 of 23

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Query Match 7,64; Score 111; DB 3; Length 969;
Best Local Similarity 51.61; P-adj No. 1, 1e-17;
Matches 380; Conservative 0; Mismatches 320; Indels 37; Gaps 4;
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Db 195 ATTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
Oy 309 ATTTATGCTTATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAA 368
Db 255 TAAAGCTGCTGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 314
Oy 369 CGATGAGTGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428
Db 315 AGATGAGATGCTTAAAGCGCTTAAAGCGCTTAAAGCGCTTAAAGCGCTTAAAGCGCTTAAAG 374
Oy 429 TTTGCTGAGCTTATTTACAGAGTATTTACAGAGTATTTACAGAGTATTTACAGAGTATTT 488
Db 375 TTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
Oy 489 AGATGCTTATTTCTTGGAGAGTCTTGGAGAGTCTTGGAGAGTCTTGGAGAGTCTTGGAGAG 548
Db 432 CATTTGAGATGCTTAAAGCGCTTAAAGCGCTTAAAGCGCTTAAAGCGCTTAAAGCGCTTAAAG 491
Oy 549 CTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
Db 492 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 551
Oy 609 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 654
Db 532 TCAATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 611
Oy 655 -----CCTTGGAGCTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
Db 612 GCGCTAGAGTGGGAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 671
Oy 713 A-----TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 755
Db 672 TACTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
Oy 756 AGAACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 815
Db 732 CGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
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SCORE Search Results Details for Application 10753267 and Search Result 20070202_145104_us-10-753-267-19.rst.

[Score Home Page](#) [Retrieval Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

[this page](#) gives you Search Results detail for the Application 10753267 and Search Result 20070202_145104_us-10-753-267-19.rst.

Go Back to previous page

GenCore version 6.2
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```

M nucleic - nucleic search, using av model
run on:      February 5, 2007, 13:38:19 : Search time 11913 Seconds
              (without alignments)
              7629.489 Million cell updates/sec

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title: US-10-753-267-19
perfect score: 1465
sequence: 1 ttggacacactggcagctcc.....gcacagtctcagctcactgc 1465

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Scoring table:  IDENTITY_MUC
                  Gapop 10.0 , Gapext 1.0
                  searched:  53585215 seqs, 31020513797 residues
                  total number of hits satisfying chosen parameters:  107170430

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inimum DB seq length: 0
maximum DB seq length: 200000000

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Cost-processing: Minimum Match 01
Maximum Match 1001
Listing first 45 summaries

Database : EST:

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2: 0b_003.
3: 0b_004.
4: 0b_005.

http://es/ScoreAccessWeb/GetItem.action?AppId=10753267&seqId=1089415&itemName=20070202_145104_us-10-753-267-19.r... 2/8/07

USCORE Search Results Details for Application 10753267 and Search Result 20070202 145104 us-10-753-267-19.rst.

[illegible]

ALIGNMENTS

[illegible]

ADJ5332 CR623543 (HUMAN).

CR623543.1 GI:50504350
UTR: CDS:IT -DNA
EYVWQNS

Source: Homo sapiens (human)

Eukaryota; Metazoa; Chori-

Caterhini: Hominidae: H

AUTHORS Li, W.B., Gruber, C., Jess

http://es/ScoreAccessWeb/CrefItem.action?AppId=10753267&seqId=1089415&itemName=2(M70202_145104_us-10-753-267-19.r... 2/8/07

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2/8/07

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8:  qb_est7.*
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17: qb_est3.*
18: qb_est4.*
19: qb_est5.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

No.	Result	Score	Query	Match	length	DB	ID	Description
1		1449.4	98.9	2081	6	CR623543		CR623543 full-length
2		1385.5	74.5	2218	6	CR805990		CR805990 Pongo pyg
3		1106.4	67.5	1749	6	CR617900		CR617900 full-length
4		1106.4	75.5	1749	6	CR617900		CR617900 full-length
5		938.4	64.1	1072	5	BX338516		BX338516 full-length
6		938.4	64.1	1545	6	CR605188		CR605188 full-length
7		931.6	62.6	991	5	BX342345		BX342345 CRX2345
8		931.6	62.6	991	5	BX342345		BX342345 CRX2345
9		912.4	62.3	962	10	CR803513		CR803513 TLINGIDZ
10		896.4	61.2	1098	5	CR398595		CR398595 CRX398595
11		892.6	60.9	1059	5	EX361718		EX361718 CRX361718
12		877.3	59.6	913	5	BX441001		BX441001 CRX441001
13		877.3	59.6	913	5	BX441001		BX441001 CRX441001
14		862.2	59.5	1068	3	CR604209		CR604209 AGCM0001
15		862.2	59.5	1068	3	CR604209		CR604209 AGCM0001
16		868.6	59.3	869	1	AL533970		AL533970 AL533970
17		854.8	58.3	923	1	AL531946		AL531946 AL531946
18		852.2	58.2	869	4	BU181695		BU181695 AGCM0001
19		845.6	57.7	1012	1	AL539470		AL539470 AL539470
20		845.6	57.7	1012	1	AL539470		AL539470 AL539470
21		842.0	57.5	1014	5	BX441949		BX441949 CRX441949
22		840.2	57.4	1013	1	AL541042		AL541042 AL541042

http://es/ScoreAccessWeb/GetItem.action?Appld=10753267&seqId=1089415&itemName=20070202_145104_us-10-753-267-19.f... 2/8/07

SCORE Search Results Details for Application 10753267 and Search Result 20070202 145104 us-10-753-267-19.rst.

JOURNAL	
REMARK	Unpublished Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ invitrogen Corporation 1600 Fardes Avenue 2 (bases 1 to 2081) Genoscope, Paris, France Submission Submitted (20-JUL-2004) Genoscope - Centre National de Séquençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqserv@genoscale.cns.fr - Web : www.genoscale.com.cn.fr) 1st strand cDNA was primed with a MscI-oligo(dT) primer. Five prime ends were sequenced from both strands. The sequence was submitted into the NCBI and EMBL v sites of the POWSAPP 6 vector. Library was normalized. Library was constructed by Life Technologies. *
COMMENT	Location/Qualifiers LOCUS=POWSPAPP_6 /accession="Homo sapiens" /mol_type="mRNA" /db_xref=taxon:"9606" /clone="CSDDM003D20" /tissue_type="testis fetal liver" /library="POWSPAPP_6"
FEATURES	source
ORIGIN	

Query Match 98.91; Score 1449.4; DB 6; Length 2081;
Best Local Similarity 99.81; Pred. No. 1,3e-295;

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61 ATTATAGGCTGTCTCGAGAGATTGAAAAATGGCAACAATGAAGATCTCAGCATCTT 120
66 ATTATAGGCTGTCTCGAGAGATTGAAAAATGGCAACAATGAAGATCTCAGCATCTT 125
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121 AGTTACGATCTCTGGCTGGGAATGTAGATGATCTTACTCTGAGAACTCTCTGCA 180
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136 GACCATCTTAAATCTCTGGAGATCTGTGGATGATGATCTTAACTACGAGATCTGCA 240
181 GACCATCTTAAATCTCTGGAGATCTGTGGATGATGATCTTAACTACGAGATCTGCA 240
196 GACCATCTTAAATCTCTGGAGATCTGTGGATGATGATCTTAACTACGAGATCTGCA 255

http://es/ScoreAccessWeb/GetItem.action?AppId=10753267&seqId=1089415&ItemName=20070202_145104_us-10-753-267-19.r...

[illegible]

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C860990.1 GI:55732788
HTC
Pongo pygmaeus (orangutan)
Pongo pygmaeus
ORGANISM
Eukaryota; Metazoa; Chordata; Creniata; Vertebrata; Euteleostomi;
Mammalia; Euarcharia; Primates; Haplorhini;
Kathartiformes; Pongidae; Pongo.
AUTHORS
Kocher, K., Beyer, A., Meves, H.W., Neill, B., Andl, C., Oanger, A.,
Fobo, G., Han, M. and Wiemann, S.
CONSTRMT
Direct Submission
TITLE
Submitted (Unpublished) 2004 MIPS, Ingolstaender Landstr.l.D-85764
JOURNAL
Nuremberg, GERMANY
COMMENT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkiz-heidelberg.de;
sequenced by BMFI (Blomendal Research Center at the
Heinrich-Heine-University, Dusseldorf/Germany) with the cDNA
sequencing consortium of the German Genome Project. This clone
is deposited in the German Gene Bank, Deutsche Sammlung von
Reagentensubstanzen fuer Genomforschung GmbH in Berlin, Germany.
Please contact RPD for ordering:
http://www.rspd.de/cgi-bin/products/c.cgi?cloneid=DNKEp459K1318
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdmv/.
FEATURES
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Ds	676	GAGAGCTATATCTTGGAGCTGAGATTTTCAATGGAGTGTGCTTTTGGTGAATCA	735
Oy	721	ATTCCTTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	780
Ds	736	ATTCCTTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	795
Oy	781	TATGATATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG	840
Ds	796	TATGATATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG	855
Oy	841	GATTCGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	900
Ds	856	GATTCGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	915
Oy	901	ATTTTGGGAGAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATG	960
Ds	916	ATTTTGGGAGAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATG	975
Oy	961	AGAGCTATATATCTTGGAGCTGAGATTTTCAATGGAGTGTGCTTTTGGTGAAT	1020
Ds	976	AGAGCTATATATCTTGGAGCTGAGATTTTCAATGGAGTGTGCTTTTGGTGAAT	1035
Oy	1021	AAATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1080
Ds	1036	AAATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1095
Oy	1081	TGATTAAGAGAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATG	1140
Ds	1096	TGATTAAGAGAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATG	1155
Oy	1141	CTACAGTCTATATATGATGATGATGATGATGATGATGATGATGATGATGATG	1200
Ds	1156	CTACAGTCTATATATGATGATGATGATGATGATGATGATGATGATGATGATG	1215

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089415&ItemName=20070202_145104_us-10-753-267-19.rsl. 28/07

SCORE Search Results Details for Application 10753267 and Search Result 20070202_145104_us-10-753-267-19.rsl. Page 11 of 23

JOURNAL	Submitted (20-JUN-2004) Genoscope - Centre National de Sequençage : BP 131 91006 EVRY cedex - FRANCE (E-mail : seq@genoscope.cns.fr)			
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pGVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.			
FEATURES	Location/Qualifiers 1..1740 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS001060709" /tissue_type="Placenta Cat 25-normalized" /plasmid="pGVSPORT_6"			
ORIGIN	Query Match 75-517; Score 1106.4; DB 6; Length 1740; Best Local Similarity 99.71; Pred. No. 4e-223; Matches 1119; Conservative 0; Mismatches 1; Indels 2; Gaps 1/			
Oy	344	AGGATAGGCGAGAGATGGGAAACCAATGGAGGTGTTCMAAGCTCTCTCTTATTC	403	
Ds	29	AGGATAGGCGAGAGATGGGAAACCAATGGAGGTGTTCMAAGCTCTCTCTTATTC	88	
Oy	404	ACTTGTGTATCAGCTGCTTATTTGTTGAGTCTATTTTACAGAGTATTTCAATA	463	
Ds	89	ACTTGTGTATCAGCTGCTTATTTGTTGAGTCTATTTTACAGAGTATTTCAATA	148	
Oy	464	TTCTTTATATGGGAAGATGGGAGATGGTATTTCTTTTGGAGAGATCTTGCTT	523	
Ds	149	TTCTTTATATGGGAAGATGGGAGATGGTATTTCTTTTGGAGAGATCTTGCTT	208	
Oy	524	GTGAGCTATTGAGATCTTGGGATATTTTCTGATAGACTCTTACACCAAGAA	583	
Ds	209	GTGAGCTATTGAGATCTTGGGATATTTTCTGATAGACTCTTACACCAAGAA	268	
Oy	584	TATACAGTATATATTAAGTCTATGATTTTGGATCTTGGAGTGTGAGTGTGAG	643	
Ds	269	TATACAGTATATATTAAGTCTATGATTTTGGATCTTGGAGTGTGAGTGTGAG	328	
Oy	644	ATATGCACTATTTGGAGACTGATCTTGGAGTGTGATTTTCTGATGATCTGTC	703	
Ds	329	ATATGCACTATTTGGAGACTGATCTTGGAGTGTGATTTTCTGATGATCTGTC	388	

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089415&ItemName=20070202_145104_us-10-753-267-19.rsl. 28/07

Oy	1201	GAGCTTTAAGAGACATGCTGCTGAGCTGAGAGAGTGTGGATGATGAGATATA	1260
Ds	1216	GAATTTTTAAGAGACATGCTGCTGAGCTGAGAGAGTGTGGATGATGAGATATA	1275
Oy	1261	ATCATGCTGCTTCTCCCAAGTAAACCATAGGCTGAAGTTCATATGGCTTTAAATC	1320
Ds	1276	ATCATGCTGCTTCTCCCAAGTAAACCATAGGCTGAAGTTCATATGGCTTTAAATC	1334
Oy	1331	TTTATGATATATGCTGATCTTCAGAAATTTCTTCATGAGTGTATGGCTTATATTA	1380
Ds	1335	TTTATGATATATGCTGATCTTCAGAAATTTCTTCATGAGTGTATGGCTTATATTA	1394
Oy	1381	ACTTTTTTTATTTTTTTTGGAGCAAGCCAGCAACTGCTGCTTGGCTGGAGTG	1440
Ds	1395	ACTTTTTTTATTTTTTTTGGAGCAAGCCAGCAACTGCTGCTTGGCTGGAGTG	1450
Oy	1441	TGCTGGCAGAGCTCAGCTCACTGC	1465
Ds	1451	TAGTGGCAGAGCTCAGCTCACTGC	1475
RESULT 3			
CR623263	1740 bp	mRNA	linear
LOCUS	full-length cDNA clone CS001060709 of Placenta Cot 25-normalized		
DEFINITION	of Homo sapiens (human)		
ACCESSION	CR623263		
VERSION	CR623263.1 GI:50504070		
KEYWORDS	HTC; CHSLT; cDNA.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1740)		
TITLE	Full-length cDNA libraries and normalization		
PMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue		
REFERENCE	2 (bases 1 to 1740)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089415&ItemName=20070202_145104_us-10-753-267-19.rsl. 28/07

SCORE Search Results Details for Application 10753267 and Search Result 20070202_145104_us-10-753-267-19.rsl. Page 12 of 23

Oy	704	TTTGTGTGATCATGATATCTCTTTGGGATGAGTGGTGTGATGATGAGACTA	763
Ds	389	TTTTGTGTGATCATGATATCTCTTTGGGATGAGTGGTGTGATGAGACTA	448
Oy	764	TTGATGTCATAGTGGTATGATATCTCTCAAGCGTTAAATGATGCTCTTCTATG	823
Ds	449	TTGATGTCATAGTGGTATGATATCTCTCAAGCGTTAAATGATGCTCTTCTATG	508
Oy	824	CTGGTCTGGGATCATGATTTCCACACATGATCTTCTGGAAGCTTGTCTCAAT	883
Ds	509	CTGGTCTGGGATCATGATTTCCACACATGATCTTCTGGAAGCTTGTCTCAAT	568
Oy	884	TTACATGGTGGATCGAATTTTGGAGAGACTCTCAGTATATGCTTATATGAAAGA	943
Ds	569	TTACATGGTGGATCGAATTTTGGAGAGACTCTCAGTATATGCTTATATGAAAGA	628
Oy	944	GGAGAGTTTGGAGAAAGAGTGAATATATCTCAGTAAAGCTCTCTGAAAGATA	1003
Ds	629	GGAGAGTTTGGAGAAAGAGTGAATATATCTCAGTAAAGCTCTCTGAAAGATA	688
Oy	1004	CTTTTCTGGAATTCAGAAAGTACTAGTACATGCTTCTGGAGAGCAAGATAGCAT	1063
Ds	689	CTTTTCTGGAATTCAGAAAGTACTAGTACATGCTTCTGGAGAGCAAGATAGCAT	748
Oy	1064	GTCTTCTGCTACTAGTGAATAAAGAGATTAACACCTTTATTAATCTTCTAGTG	1123
Ds	749	GTCTTCTGCTACTAGTGAATAAAGAGATTAACACCTTTATTAATCTTCTAGTG	808
Oy	1124	GACTTTTCTACTTACTAGTCAAGTCTATATATGTAAGAAATGAATATATATTA	1183
Ds	809	GACTTTTCTACTTACTAGTCAAGTCTATATATGTAAGAAATGAATATATTA	868
Oy	1184	AGTACATGTTTCATGAGGAGTGTTAAAGACCATGTTCTAGCTTCCAGAGGTTT	1243
Ds	869	AGTACATGTTTCATGAGGAGTGTTAAAGACCATGTTCTAGCTTCCAGAGGTTT	928
Oy	1244	GGATACATGAGATATATCTATCTATGCTTTTCTCCAGTAAACATAGGCTGAGTCA	1303
Ds	929	GGATACATGAGATATATCTATCTATGCTTTTCTCCAGTAAACATAGGCTGAGTCA	988
Oy	1304	CATTGGGCTTTAAATCTTTTATGATATATGCTGCTTCTGAGAAATTTCTCATAGTG	1363
Ds	989	CATTGGGCTTTAAATCTTTTATGATATATGCTGCTTCTGAGAAATTTCTCATAGTG	1048

http://es.ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089415&ItemName=20070202_145104_us-10-753-267-19.rsl. 28/07

RESULT 7
BX342345
DEFINITION
BX342345 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS00K012Y106 5-PRIME, mRNA sequence.
BX342345
VERSION
BX342345.2 GI:46272279
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Eucelostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhina;
Catherhini; Hominoidea; Homo.
1 (bases 1 to 991)
Li.W.B., Gruber.C., Jassse.J. and Polayes.D.
Full-length cDNA libraries and normalization
Oupublishing (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seq@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the pCMVSPORT 6 vector. Library was normalized. Library was
divided into 10 pools. This sequence belongs to sequence cluster
2372.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?se=CS00K0128603P1ce=2372.f.
Location/Qualifiers
1..991 name="Homo sapiens"
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/cotton="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

http://es/ScoreAccessWeb/CellItem.action?AppId=10753267&seqId=1089415&ItemName=20070202_145104_us-10-753-267-19.r... 2/8/07

SCORE Search Results Details for Application 10753267 and Search Result 20070202_145104_us-10-753-267-19.rst.

Page 23 of 23

Oy 1116 CCTAGTGGAGCTTTTCTACCTTACAGAGTCTATATATGTAGAAATGATTAATA 1175
Db |||||||
Oy 604 CCTAGTGGAGCTTTTCTACCTTACAGAGTCTATATATGTAGAAATGATTAATA 663
Db |||||||
Oy 1176 TATATTAGTACAGTTTCTACAGAGTTTAAAGAGAGTCTGTAGCTGCAG 1235
Db |||||||
Oy 664 TATATTAGTACAGTTTCTACAGAGTTTAAAGAGAGTCTGTAGCTGCAG 723
Db |||||||
Oy 1236 AAGGTTTGGATAGAGTATATCTATGGCTTTCTCCAGTAAACCATAGGCT 1295
Db |||||||
Oy 724 AAGGTTTGGATAGAGTATATCTATGGCTTTCTCCAGTAAACCATAGGCT 783
Db |||||||
Oy 1296 GAAGTTTGCATCTGGCTTTAAATCTTTTATAGATATATCTGTAGAAATCT 1355
Db |||||||
Oy 784 GAAGTTTGCATCTGGCTTTAAATCTTTTATAGATATATCTGTAGAAATCT 843
Db |||||||
Oy 1356 CATAGTGTATGGCTTATATTAATCTTTTATTTTATTTTGTAGAAAGCCAA 1415
Db |||||||
Oy 844 CATAGTGTATGGCTTATATTAATCTTTTATTTTATTTTGTAGAAAGCCAA 902
Db |||||||

BLAST 2.2.8

Score 11.86, E-value: 1.01E-05

ORIGIN
Query Match 63.6%; Score 931.6; DB 5; Length 991;
Best Local Similarity 99.3%; Pred. No. 3.5e-186;
Matches 943; Conservative 3; Mismatches 2; Indels 1;
Oy 516 CTTTGGTGGAGCTATTAAGATCTTGGCACTATTTCGTGATAGACTTTACACA 575
Db |||||||
Oy 4 CTTTGGTGGAGCTATTAAGATCTTGGCACTATTTCGTGATAGACTTTACACA 63
Db |||||||
Oy 576 CAAAGATATACAGTATATTCATAAGTTCATGATGAGTTTCAGGCTCATTGGAAT 635
Db |||||||
Oy 64 CAAAGATATACAGTATATTCATAAGTTCATGATGAGTTTCAGGCTCATTGGAAT 123
Db |||||||
Oy 636 GGAAGCTGATATGCAAGCTTTGGAGACTCTAATCTTGGAGCTGATTTTCATG 695
Db |||||||
Oy 124 GGAAGCTGATATGCAAGCTTTGGAGACTCTAATCTTGGAGCTGATTTTCATG 183
Db |||||||
Oy 696 AATCGCTTTTGTGTGATCATGATTCCTTCTGGCATGGGTGACATTCGTTATT 755
Db |||||||
Oy 184 AATCGCTTTTGTGTGATCATGATTCCTTCTGGCATGGGTGACATTCGTTATT 243
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Oy 756 AGAAGTATTAAGCTGATGAGTTCATGATGAGTTCATGAGCTTAAATCTGATCC 815
Db |||||||
Oy 244 AGAAGTATTAAGCTGATGAGTTCATGATGAGTTCATGAGCTTAAATCTGATCC 303
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Oy 816 TTTCTATCTGCTTCTGGGATCATGATTTCCACACATGAACTTCATTTGGAATATGC 875
Db |||||||
Oy 304 TTTCTATCTGCTTCTGGGATCATGATTTCCACACATGAACTTCATTTGGAATATGC 363
Db |||||||
Oy 876 TTCAGCTTTACAGTGGGATGCAATTTTGGAGAGACTCTGATATATGGCTATTA 935
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Oy 364 TTCAGCTTTACAGTGGGATGCAATTTTGGAGAGACTCTGATATATGGCTATTA 423
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Oy 936 TGAAGAGAGAGAGAGTTTGAAGAAAGCTGATTAATATCTCAAGTAAAGCTTCTGA 995
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Oy 424 TGAAGAGAGAGAGAGTTTGAAGAAAGCTGATTAATATCTCAAGTAAAGCTTCTGA 483
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Oy 484 AAGATAAAGCTTTCTGATTCAGAGAACTAGTACATCTGCTGAGAGAGAGAA 543
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Oy 1056 ATAGGATGCTCTCTGGCTACTAGTAAAGTAAAGAGAGATTAAGAGCTTTAATACCT 1115
Db |||||||
Oy 544 ATAGGATGCTCTCTGGCTACTAGTAAAGTAAAGAGAGATTAAGAGCTTTAATACCT 603
Db |||||||

http://es/ScoreAccessWeb/CellItem.action?AppId=10753267&seqId=1089415&ItemName=20070202_145104_us-10-753-267-19.r... 2/8/07

SCORE Search Results Details for Application 10753267 and Search Result 20070202_145101_us-10-753-267-19.rge.

Score Home Page Refidive Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10753267 and Search Result 20070202_145101_us-10-753-267-19.rge.

Start | Next | Back

Go Back to previous page

On nucleic - nucleic search, using sw model

Run on: February 5, 2007, 13:28:04 : Search time 9179 Seconds (Without alignments)
11031.837 Million cell updates/sec

File: US-10-753-267-19
Profile score: 1465
Sequences: 1 tggacacacgcgcaccc.....gcacgcgcgcacgcgcgc 1465

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 7565341 seqs, 3456014813 residues
Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 01
Maximum Match 1001
Listing first 43 summaries

Database : GenEmbl:
1: gb_envi:
2: gb_pat:
3: gb_ph:
4: gb_pl:
5: gb_pr:

RC006802 Mus muscu
AF011350 Homo sapi
AF196983 Homo sapi
AF197004 Pan trogl
AC152151 Dasytus n
AJ719718 Gallus ga
DD666794 Nucleic A
BC121156 Emerico t
BV321156 Emerico t
BC050163 Danio rer
AX885298 Sequence
BD024908 Sequence
AR725169 Sequence
AC011570 Homo sapi
DD666085 Nucleic A
DD666531 Nucleic A
BV417371 322966271
BV650629 521796375
BV650204 521796820

RESULTS
HSU93162 1465 bp mRNA linear PRI 24-OCT-1997
DEFINITION Homo sapiens C4-sterol methyl oxidase homolog (DES34) mRNA.
complete cds.
ACCESSION U93162.1 GI:1930074
VERSION U93162.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhina;
Cathartini; Hominoidea; Homo.
Homo sapiens (to 1465)
Direct Submission
TITLE Submitted (11-MAR-1997) Abteilung Medizinische Genetik,
Kinderpoliklinik der LMU, Muenchen, Goethestrasse 29, Muenchen
D-80336, Germany
JOURNAL
COMMENT A pseudogene (DES34P1) has been isolated by K. Hermann on

6: gb_ro:
7: gb_ro:
8: gb_ro:
9: gb_ro:
10: gb_ro:
11: gb_ro:
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13: gb_ro:
14: gb_ro:
15: gb_ro:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result	No.	Score	Match	Length	DB	ID	Description
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	2	1467.8	98.8	1741	2	CS16341	CS16341 Sequence
	3	1467.8	98.8	1741	2	DD223014	DD223014 Genes for
	4	1416.4	96.7	1744	2	CQ715218	CQ715218 Sequence
	5	1416.4	96.7	2217	5	BC107879	BC107879 Homo sapi
	6	1383.4	94.4	1944	5	BC010653	BC010653 Homo sapi
	7	1376.6	94.0	1751	2	CS351308	CS351308 Sequence
	8	1376.6	94.0	1751	2	DD200087	DD200087 Methods a
	9	1376.6	94.0	1751	2	AD782837	AD782837 Sequence
	10	1376.6	94.0	1751	2	AD782837	AD782837 Sequence
	11	1376.6	94.0	1751	5	AB169205	AB169205 Homo methy
	12	1376.6	94.0	1751	5	AB169840	AB169840 Macaca fa
	13	860.6	58.7	1170	14	AY370690	AY370690 Sus acrofi
	14	783.2	53.5	1560	5	HSU93261	U93261 Homo sapien
	15	783.2	53.5	337101	5	HSXK6RPR	AL121578 Homo sapi
	16	780	53.2	144722	5	AC160052	AC160052 Pan trogl
	17	780	53.2	192593	5	AC184690	AC184690 Pan trogl
	18	763.2	52.1	1712	2	CS163932	CS163932 Sequence
	19	763.2	52.1	1712	2	DD370486	DD370486 Sequence
	20	763.2	52.1	1712	2	DD317449	DD317449 Primary R
	21	763.2	52.1	1712	6	D50559	D50559 Rattus norv
	22	763.2	52.1	1728	6	BC063155	BC063155 Rattus no
	23	763.2	52.1	1733	2	AB827434	AB827434 Sequence
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	25	763.2	52.1	1733	2	E12625	E12625 cDNA encodi

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FEATURES
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Ds	661	GAGACTTAATCTTTCGGAAGCTGATTTTCATGGAATGAGTGGCTTTTGTGTGATCACTA	720
Oy	721	ATGCTGTGGGAGCTGGGAGCTGATGCTTTATAGAACTATGATGCTGCTAGTGGT	780
Ds	721	ATGCTGTGGGAGCTGGGAGCTGATGCTTTATAGAACTATGATGCTGCTAGTGGT	780
Oy	781	TATGATATCTCTCAAGCTTTTAAATCTGATCTTCTATGCTGTCTGCGCATCAT	840
Ds	781	TATGATATCTCTCAAGCTTTTAAATCTGATCTTCTATGCTGTCTGCGCATCAT	840
Oy	841	GATTTCGAGCAGATGATGCTGATGGAAGCTGCTTCAACATTTAGATGCTGGAGTGA	900
Ds	841	GATTTCGAGCAGATGATGCTGATGGAAGCTGCTTCAACATTTAGATGCTGGAGTGA	900
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Ds	901	ATTTTGGAGAGAGCTTCAGTATATGCTGATATGAAAGAGGAAGAAGTTTGAGAA	960
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Ds	1021	AAAGTGTAGCTAACATGCTTCTGGAGAGAGAAATAGCATGCTCTTGGCTACTAAG	1080
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http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1189414&ItemName=20070202_145101_us-10-753-267-19.rgc 28/07

SCORE Search Results Details for Application 10753267 and Search Result 20070202_145101_us-10-753-267-19.rgc. Page 11 of 23

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		Matches 146; Conservative 0; Mismatches 2; Indels 2; Gaps 1;	
Oy	1	TTGGAAACCTGGCGAGCTCTGGGTCTGGTGGCGGAGCTATCTCGCGCGCTTCAGA	60
Ds	1	TTGGAAACCTGGCGAGCTCTGGGTCTGGTGGCGGAGCTATCTCGCGCGCTTCAGA	60
Oy	61	ATTAAGAGCTGTGGAGATTTGGAATATGGAATGGCAAGATGAGAGTGTGATG	120
Ds	61	ATTAAGAGCTGTGGAGATTTGGAATATGGAATGGCAAGATGAGAGTGTGATG	120
Oy	121	AGTTCAGATCTCTGGCTGGGAATATGATATCACTTTTACGTGAATCTCTGCA	180
Ds	121	AGTTCAGATCTCTGGCTGGGAATATGATATCACTTTTACGTGAATCTCTGCA	180
Oy	181	GACATTTAAATATGCTGGATATGGAATATGGAATATGGAATATGGAATATGGA	240
Ds	181	GACATTTAAATATGCTGGATATGGAATATGGAATATGGAATATGGAATATGGA	240
Oy	241	ACATGGGATCTCTTATAGTTCATGAGCCCTTATCTTCTTATCTTCTGCTGAT	300
Ds	241	ACATGGGATCTCTTATAGTTCATGAGCCCTTATCTTCTTATCTTCTGCTGAT	300
Oy	301	TTATTCATTTATGCTATATGGAATATGGAATATGGAATATGGAATATGGAAT	360
Ds	301	TTATTCATTTATGCTATATGGAATATGGAATATGGAATATGGAATATGGAAT	360
Oy	361	TGGGAAGCACTGGAAGTCTTCAAGTCTCTCTTTATCATCTCTGATTCAGCTG	420
Ds	361	TGGGAAGCACTGGAAGTCTTCAAGTCTCTCTTTATCATCTCTGATTCAGCTG	420
Oy	421	CTTTCATTTCTGGAGCTATTTTACAGATATTCATATCTTATGATGGGAA	480
Ds	421	CTTTCATTTCTGGAGCTATTTTACAGATATTCATATCTTATGATGGGAA	480
Oy	481	AGATGCTCAGATGCTATTTCTTGGCAGAGTCTTTGGTGTGCAAGTATGAGAT	540
Ds	481	AGATGCTCAGATGCTATTTCTTGGCAGAGTCTTTGGTGTGCAAGTATGAGAT	540

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1189414&ItemName=20070202_145101_us-10-753-267-19.rgc 28/07

Oy	1201	GAGCTTTAAAGACATGCTTCTTACGCTTCAGAGAGGTTTGGATCATAGAGTATA	1260
Ds	1201	GAGCTTTAAAGACATGCTTCTTACGCTTCAGAGAGGTTTGGATCATAGAGTATA	1260
Oy	1261	ATCTATGCTTCTTCTCCAGTAAACATAGGCTCGAGTTCACATCGGCTCTTAAATC	1320
Ds	1261	ATCTATGCTTCTTCTCCAGTAAACATAGGCTCGAGTTCACATCGGCTCTTAAATC	1320
Oy	1321	TTTATGATATGCTGCTATCTGCAAGATTAAGCTTCTATGCTGCTGCTGCTGCTA	1380
Ds	1321	TTTATGATATGCTGCTATCTGCAAGATTAAGCTTCTATGCTGCTGCTGCTGCTA	1380
Oy	1381	ACTTTTATTTATTTTATTTTATGAGCAAGGCAACAGCTCTGCTGCTGCTGCTGCTG	1440
Ds	1381	ACTTTTATTTATTTTATTTTATGAGCAAGGCAACAGCTCTGCTGCTGCTGCTGCTG	1440
Oy	1441	TGGTGGCAGCTCTCAGCTCACTGC	1463
Ds	1439	TGGTGGCAGCTCTCAGCTCACTGC	1463
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D0223014			
LOCUS 1741 bp DNA linear PAT 18-MAR-2006			
DEFINITION Genes for diagnosing colorectal cancer.			
ACCESSION D0223014			
VERSION D0223014.1 GI:90081623			
KEYWORDS JP 2005229928-A/138.			
SOURCE Homo sapiens (human)			
ORGANISM			
Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Hominoidea; Homo.			
REFERENCE			
1 (bases 1 to 1741)			
AUTHORS Yuan W.Z. and Hu L.X.			
TITLE Genes for diagnosing colorectal cancer.			
JOURNAL Patent: JP 2005229928-A 138 02-SEP-2005;			
COMMENT			
PN JP 2005229928-A/138			
PD 02-SEP-2005			
PF 20-FEB-2004 JP 200404186			
CC PI wang zhao yuan.lin xiu zu			
PH Key Location/Qualifiers.			

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SCORE Search Results Details for Application 10753267 and Search Result 20070202_145101_us-10-753-267-19.rgc. Page 12 of 23

Ds	481	AGATGCTCAGATGCTATTTCTTTGGCAGAGCTCTTGTGTGCGATATTGAGAT	540
Oy	541	ACTTGGCACTATTTTCGATGAGCTTACAGCAAGATATACAGTATTCAT	600
Ds	541	ACTTGGCACTATTTTCGATGAGCTTACAGCAAGATATACAGTATTCAT	600
Oy	601	AAAGTTCATGAGTTTCAGGCTCCATTTGGAAATGGAAGCTGAATACGACATCTTG	660
Ds	601	AAAGTTCATGAGTTTCAGGCTCCATTTGGAAATGGAAGCTGAATACGACATCTTG	660
Oy	661	GAGACTTAATCTTTCGGAAGCTGATTTTCATGGAATGAGTGGCTTTTGTGTGATCACTA	720
Ds	661	GAGACTTAATCTTTCGGAAGCTGATTTTCATGGAATGAGTGGCTTTTGTGTGATCACTA	720
Oy	721	ATCTCTTGGGAGCTGGTGGAGCTGTTATTAGAACTATGATGCTGCTAGTGGT	780
Ds	721	ATCTCTTGGGAGCTGGTGGAGCTGTTATTAGAACTATGATGCTGCTAGTGGT	780
Oy	781	TATGATATCTCTCAAGCTTTAAATCTGATCTTCTATGCTGCTTCTGCGCATCAT	840
Ds	781	TATGATATCTCTCAAGCTTTAAATCTGATCTTCTATGCTGCTTCTGCGCATCAT	840
Oy	841	GATTTCGAGCAGATGATGCTTCAACATTTAGATGCTGGAGTGA	900
Ds	841	GATTTCGAGCAGATGATGCTTCAACATTTAGATGCTGGAGTGA	900
Oy	901	ATTTTGGAGAGAGCTTCAGTATATGCTGATATGAAAGAGGAAGAAGTTTGAGAA	960
Ds	901	ATTTTGGAGAGAGCTTCAGTATATGCTGATATGAAAGAGGAAGAAGTTTGAGAA	960
Oy	961	AGAGCTGAATATCTGAGTAAAGCTTCTGGAAGTAAAGCTTCTGGAATTCAG	1020
Ds	961	AGAGCTGAATATCTGAGTAAAGCTTCTGGAAGTAAAGCTTCTGGAATTCAG	1020
Oy	1021	AACTAGTACTAGATGCTTCTGGAGAGAGAAATAGCATGCTCTTGGCTACTAAG	1080
Ds	1021	AACTAGTACTAGATGCTTCTGGAGAGAGAAATAGCATGCTCTTGGCTACTAAG	1080
Oy	1081	TCATTAAGAGATATACAGCTGTATATAGCTGCTTAAGCTGCTAGGGAAGTTTTCAGTTA	1140
Ds	1081	TCATTAAGAGATATACAGCTGTATATAGCTGCTTAAGCTGCTAGGGAAGTTTTCAGTTA	1140
Oy	1141	CCTACAGTCTATATATGAGAAATGAATATATATTAAGTACAGTTTTCATCAG	1200
Ds	1141	CCTACAGTCTATATATGAGAAATGAATATATATTAAGTACAGTTTTCATCAG	1200

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089414&ItemName=20070202_145101_us-10-753-267-19.rgc 28/07

Oy	1201	GAGGTTTAAAGACATGCTTCAGCTTCAGAGAGTTTGGTACTAGAGATTATA	1260
Ds	1201	GAGGTTTAAAGACATGCTTCAGCTTCAGAGAGTTTGGTACTAGAGATTATA	1260
Oy	1261	ATCTATGGCTTTCTCCAGCTTAAGACATAGGCTGAGTTCAGATGGCTTTAAATC	1320
Ds	1261	ATCTATGGCTTTCTCCAGCTTAAGACATAGGCTGAGTTCAGATGGCTTTAAATC	1320
Oy	1321	TTTGAATATATAGTCTGCTTCAAGAAATCTCTCATAGTGTATGGCTTATATTA	1380
Ds	1321	TTTGAATATATAGTCTGCTTCAAGAAATCTCTCATAGTGTATGGCTTATATTA	1380
Oy	1381	ACTTTTATATATATTTTATGAGAGCAACCACTGCTGCTGCTGGAGTC	1440
Ds	1381	ACTTTTATATATATTTTATGAGAGCAACCACTGCTGCTGCTGGAGTC	1440
Oy	1441	TGCTGGACAGCTGACCTCACTGC 1465	
Ds	1439	TGCTGGACAGCTGACCTCACTGC 1463	
RESULT 4			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
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ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			

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SCORE Search Results Details for Application 10753267 and Search Result 20070202_145101_us-10-753-267-19.rge

Ds	541	GATCTGGCAGCTATTTCTGCTAGCTTTACACGACAAAGATATACAGTATAT	600
Oy	598	CATAAAGTATCATAGTTTTCAGCTGCTCATTTGGATGGAGCTGATATGACATCT	657
Ds	601	CATAAAGTATCATAGTTTTCAGCTGCTCATTTGGATGGAGCTGATATGACATCT	660
Oy	658	TTGAGAGCTCATTTTTCAGAGCTGATTTTCAGAGCTGATTTTCAGAGCTGAT	717
Ds	661	TTGAGAGCTCATTTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTG	720
Oy	718	GTATCTCTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTT	777
Ds	721	GTATCTCTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTT	780
Oy	778	GCTTATGATATCTCTCTCACTGCTTTCAGAGCTGATTTTTCAGAGCTGATTT	837
Ds	781	GCTTATGATATCTCTCTCACTGCTTTCAGAGCTGATTTTTCAGAGCTGATTT	840
Oy	838	CATGATTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTTTC	897
Ds	841	CATGATTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTTTC	900
Oy	898	CGATTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAG	957
Ds	901	CGATTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAG	960
Oy	958	AAAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTG	1017
Ds	961	AAAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTG	1020
Oy	1018	CAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTG	1077
Ds	1021	CAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTG	1080
Oy	1078	AAGTATTAAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAG	1137
Ds	1081	AAGTATTAAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAG	1140
Oy	1138	TTAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGAT	1197
Ds	1141	TTAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGAT	1200
Oy	1198	GAGGAGCTTTTAAAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTT	1257
Ds	1201	GAGGAGCTTTTAAAGAGCTGATTTTTCAGAGCTGATTTTTCAGAGCTGATTT	1260

http://es/ScoreAccessWeb/CelItem.action?AppId=10753267&seqId=1089414&ItemName=20070202_145101_us-10-753-267-19.rge

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Oy	1	TTGGACAGCTGGAGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	60
Ds	1	TTGGACAGCTGGAGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	60
Oy	61	ATTATAGCTGCTGCGAGAGATTGAAAATGGCAACAAATGAAGTGTGACATCTT	120
Ds	61	ATTATAGCTGCTGCGAGAGATTGAAAATGGCAACAAATGAAGTGTGACATCTT	120
Oy	121	AGTTAGAGCTGCTGCGAGAGATTGAAAATGGCAACAAATGAAGTGTGACATCT	179
Ds	121	AGTTAGAGCTGCTGCGAGAGATTGAAAATGGCAACAAATGAAGTGTGACATCT	180
Oy	180	AG-AACATTTAAATATCTTGGAGCTATATGTTGAATATATACAAAGTTCAG-ATT	237
Ds	181	AGAACATTTAAATATCTTGGAGCTATATGTTGAATATATACAAAGTTCAGATT	240
Oy	238	GCACATGGGATGCTTATAGTCTGAGAGCTTTATTTCTATCTGTTTACTGGA	297
Ds	241	GCACATGGGATGCTTATAGTCTGAGAGCTTTATTTCTATCTGTTTACTGGA	300
Oy	298	TTTTTATTTGAATTTACCTTATATGAAAATATGAAAATTCAGAAATGAGTACG	357
Ds	301	TTTTTATTTGAATTTACCTTATATGAAAATATGAAAATTCAGAAATGAGTACG	360
Oy	358	ACATGGGAAACCATGAGAGTGTTCAGAGCTTCTCTCTTATCTGCTGTATCAG	417
Ds	361	ACATGGGAAACCATGAGAGTGTTCAGAGCTTCTCTCTTATCTGCTGTATCAG	420
Oy	418	CTGCTTTGATTTGGAGCTTATTTTACAGAGTATTTTACAGAGTATTTCTTATG	477
Ds	421	CTGCTTTGATTTGGAGCTTATTTTACAGAGTATTTTACAGAGTATTTCTTATG	480
Oy	478	GAAGATGCGAGAGTGTATTTCTTTTGGCAGATGCTTGTGTGAGCATGGA	537
Ds	481	GAAGATGCGAGAGTGTATTTCTTTTGGCAGATGCTTGTGTGAGCATGGA	540
Oy	538	GATCTGGAGCTATTTCTGAGTACGCTTACAGCAACAAAGATATACAGTATAT	597

BC107879	2217 bp	mRNA	linear	PR1 21-JUL-2006
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				

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Mammalia: Eutheria: Euarchontoglires: Primates: Haplorhini:				
Hominidae: Homo:				
Homo sapiens (human)				
Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,				
Klausner, R.D., Collins, F.S., Wagner, L., Shenn, C.M., Schuler, G.D.,				
Altschul, S.F., Beberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,				
Hopkins, R.F., Jordan, H., Noote, T., Max, S.I., Wang, J., Hsieh, F.,				
Diachenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L.,				
Sapich, K., Bhat, N.K., Bonaldo, M.F., Casavant, T.L.,				
Carroll, P., Prange, C., Rada, S., Loque, L., N.A., Petros, G.J.,				
Abraham, R.D., Mullen, S.J., Bosak, S.A., McEwen, P.J.,				
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,				
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Ruyk, S.W.,				
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,				
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